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                         121 DIYAMKVWKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
                                                                                                                                                           241 GSAAKWNSNKWVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
                                                                                                                                                                                241 GSAAKANSNKAVNAKLPIGTPDYMAPEVLTVANGDGKGTYRLDCDWWSVGVIAYEMIYGR 300
                                                                                                                                                                                                                                                               301 SPFAEGTSARTFWNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
                                                                                                                                                                                                                                                                                                                      361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
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DIYAMKVWKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKWHLYLVWEYQPGG 180
                                                                                                                                                                                                                                        SPFAEGTSARTFINIMNFORFLKFPDDPKVSSDFLDLIOSLLCGOKERLKFEGLCCHPFF 360
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                                                                             DLLSLLNRYEDQLDENL1QFYLAEL1LAVHSVHLMGYVHRD1KPEN1LVDRTGH1KLVDF
                                                                                                    181 DLLSLINRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
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PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PELING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
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Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A
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Spytek, Kimberly A.
Edinger, Shlomit R.
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Leach, Martin D.
Agee, Michele L.
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Malyankar, Uriel M.
Ort, Tatiana
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Anderson, David W.
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Catterton, Elina
Ji, Weizhen
Miller, Charles E.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Li, Li
121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-
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Pred. No. 4.9e-189;
1; Mismatches 1; Indels 0
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OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                   GANDHI, Ameena R.
TRIBOULEY, Catherine M.
CHAWLA, Narinder K.
YAO, Monique G.
LU, Dyung Aina M.
GREENWALD, Sara R.
RAMKUWAR, Jayalaxmi
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APPLICANT: ELLIOTY, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
                                                      Sequence 7, Application US/10311034 Publication No. US20040023242A1 GENERAL INFORMATION:
                                                                                                               APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BANDWAN, Olga
APPLICANT: BOROWSKY, Mark L.
APPLICANT: AL-YOUNG, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHAH, Farrah A.
RECIPON, Shirley A.
AZIMZAI, Yalda
POLICKY, Jennifer L.
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TANG, Y. Tom
BARDER.
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Best Local Similarity 99.6
Matches 495; Conservative
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SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 497
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ORGANISM: Homo sapiens
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APPLICANT: Yu, Xuanchuan
APPLICANT: Yu, Xuanchuan
APPLICANT: Wiranda, Maricar
APPLICANT: Wiranda, Maricar
APPLICANT: Fiddle, Carl Johan
TITLE OF INVENTION: No. US20020123622Alel Human Kinases and Polynucleotides Encoding t
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
PRIOR PILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
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                                                                                                                                                                                                                                     Score 2440; DB 13;
Pred. No. 6.3e-177;
2; Mismatches 0;
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99.6%; Pred. No. 6.7e-177;
iive 2; Mismatches 0;
     PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/10028946; Publication No. US20020123622A1; GENERAL INFORMATION:
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Best Local Similarity 99.6%;
Matches 466; Conservative
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Best Local Similarity 99.69
Matches 466; Conservative
                                                                                                                                   TYPE: PRT
ORGANISM: homo sapiens
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ORGANISM: homo sapiens
                                                                                                              LENGTH: 1958
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US-10-028-946-2
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Publication No. US20020123622A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yu kuanchuan
APPLICANT: Friddle, Carl Obhan
TITLE OF INVENTION: No. US20020123622A1e1 Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/28,946
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.8%; Score 2440; DB 15; Length 623; 99.6%; Pred. No. 1.5e-177; tive 2; Mismatches 0; Indels 0
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PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PRIOR PRIORING NUMBER: 60/33,260
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2001-10-05
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Matches 466; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-10-262-511-4
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APPLICATION NUMBER: US 60/244,068
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ORGANISM: Homo sapiens
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DLLSLLARYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                                            ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
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FILE REFERENCE: 91-0262 USN
CURRENT APPLICATION NUMBER: US/10/415,011
CURRENT FILING DATE: 2003-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/USO1/47728
FILING DATE: 2001-10-20
APPLICATION NUMBER: US 60/242,410
FILING DATE: 2000-10-20
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BANDWAN, Olga
FRIBOULEN, Catherine M.
LAL, Preeti G.
RECIPON, Shirley A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 21, Application US/10415011; Publication No. US20040053394A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: INCYTE CORPORATION
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: BAUGHN, Mariah R.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: XU, Yuning
APPLICANT: ARVIZU, Chandra S.
APPLICANT: YAO, MONIQUE G.
APPLICANT: YAO, MONIQUE G.
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BOROWSKY, Mark L.
THORNTON, Michael B.
SWARNAKER Anita
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HAFALIA, April J.A.
NGUYEN, Danniel B.
GANDHI, Ameena R.
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KHAN, Farrah A.
ISON, Craig H.
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US20020160483A1el Human Myotonic Dystrophy Type Prot
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PUDLICATION No. US2020160483A1
GENERAL INFORMATION:
TITLE OF INVENTION: 13245, A No. US2020160483A1,
TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-57U1
CURRENT APPLICATION NUMBER: US/10/017,216
GURRENT APPLICATION NUMBER: US/23
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/245,708
PRIOR APPLICATION NUMBER: US 60/247,672
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/249,565
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL PROGRAM
LENGTH: 2054
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121 DIYAMKVWKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLMEEYQPGG 180
                                                                                   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQESAKDFEVRSLVGCGHFAEVQVVREKATG
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Publication No. US20040197825A1
GENERAL INFORMATION:
APPLICANT: Karicheti, Venkateswarlu
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Eliasof, Scott D.
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US-10-325-490-12
i Sequence 12, Application US/10325430
j Publication No. US20030153525A1
j GENERAL INFORMATION:
j APPLICANT: Millennium Pharmaceuticals, Inc
j APPLICANT: Millennium Pharmaceuticals, Inc
j APPLICANT: Millennium Pharmaceuticals, Inc
j TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
j TITLE OF INVENTION: 32838,336 and 52908
j FILE REFERENCE: MPI01-294PIRNM
j CURRENT APPLICATION NUMBER: US/10/325,430
j CURRENT FILING DATE: 2001-12-19
j PRIOR PELLING DATE: 2001-12-19
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99.1%; Pred. No. 3.9e-176;
iive 3; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 2053
                  2.1
                                                                                                                                                              Matches 464; Conservative
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver.
SEQ ID NO 2
                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-216-2
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ORGANISM: Homo Sapiens
US-10-325-430-12
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Pred. No. 2.9e-175;
3; Mismatches 1;
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PRIOR FILING DATE: 2003-09-26

NUMBER OF SEQ ID NOS: 136

SCHWARE: FastSEQ for Windows Version 4.0

LENGTH: 2053

TYPE: PRT

ORGANISM: Homo sapiens
US-10-757-262-52
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APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rekuda, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Shawets, Richard A
APPLICANT: Shawets, Richard A
APPLICANT: Shawets, Richard A
APPLICANT: Shawets, Richard A
APPLICANT: 21402-124
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CURRENT FILING DATE: 2001-09-26
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PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR PELING DATE: 2000-09-27
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PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
APPLICANT: Glose, Milliam
APPLICANT: Grose, Milliam
APPLICANT: Lepley, Denise M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ## APPLICANT: SINIEWEER, RICHARID A.

## APPLICANT: Rothenberg, Martin D.

## APPLICANT: Beach, Martin D.

## APPLICANT: Berges, Constance

## TILE REPERENCE: 21402-4462C

**CURRENT APPLICATION NUMBER: 06/326,483

## RIOR PELLING DATE: 2001-10-02

## RIOR PELLING DATE: 2001-10-03

## RIOR APPLICATION NUMBER: 60/337,917

## RIOR APPLICATION NUMBER: 60/327,917

## RIOR APPLICATION NUMBER: 60/327,917

## RIOR APPLICATION NUMBER: 60/328,029

## RIOR PELLING DATE: 2002-05-16

## RIOR PELLING DATE: 2002-05-16

## RIOR PELLING DATE: 2002-05-16

## RIOR APPLICATION NUMBER: 60/381,038

## RIOR APPLICATION NUMBER: 60/373,260

## RIOR PELLING DATE: 2002-04-19

## RIOR PELLING DATE: 2001-10-05

## RIOR PELLING 
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Best Local Similarity 98.9%; Pred. No. 8.4e-175;
Matches 463; Conservative 3; Mismatches 1; Indels
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
                       Malyankar, Uriel M.
                                                                                                                               Zerhusen, Bryan D.
Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets, Richard
                                                                                                                                                                                                        Zhong, Mei
Catterton, Elina
                                                             Ort, Tatiana
Gorman, Linda
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US-10-262-511-2
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PRIOR APPLICATION NUMBER: 60/238,321
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,399
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
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PRIOR FILING DATE: 201-07-12
SOFTWARRE: PALENTING DATE: 201-07-12
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Publication No. US20040038223A1
GENERAL INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-956-11
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                                                                          Score 2412.5; DB 11; Length 2066;
Pred. No. 8.5e-175;
3; Mismatches 1; Indels 1; (
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                                                                               Query Match 92.7%;
Best Local Similarity 98.9%;
Matches 463; Conservative
  ; ORGANISM: Homo sapiens
US-09-964-956-9
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Job time : 148 secs
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241 GSAAKMNSNK-VNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 299
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Sequence 1 Sequence 7 Sequence 7

Scoring table;

Database

Result No.

Perfect score:

6

Sequence:

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Sequence 2, Application US/09804471A
Patent No. 6479269.
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: 18/09/804,471A
TITLE OF INVENTION: 18/09/804,471A
TITLE OF INVENTION: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 497
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181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
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Matches 497; Conservative
  TYPE: PRT
ORGANISM: Human
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Sequence 59, Appli
Sequence 59, Appli
Sequence 62, Appli
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1 MLKFKYGARNPLDAGAAEPI......CSRILPSVYAKGSARGRCWL
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(c) 1993 - 2005 Compugen Ltd.
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US-09-916-204-4
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Sequence 2, Application US/10238709

Patent No. 6680188

GENERAL INFORMATION:

APPLICANT: WEBSTER, Maxion et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO01164DH 10/238, 709

CURRENT APPLICATION NUMBER: US/10/238, 709

CURRENT FILING DATE: 2002-09-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                               ECSQPALMKIKHVSNFVRKYSDTIAELQBLQPSAKDFEVRSLVGCGHPAEVQVVREKATG 120
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                            421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
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Best Local Similarity 100.
Matches 497; Conservative
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; ORGANISM: Human
US-10-238-709-2
                                                                                                                                                            RESULT 2
US-10-238-709-2
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APPLICANT: Miranda, Maricar
APPLICANT: Fiddle, Carl Johan
TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US 60/258,335
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGHIA: 1958
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Batent No. 6734009
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Priddle, Carl Johan
TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polymucleotides Encoding the Same
RILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION WUMBER: US 60/258,335
PRIOR PILING DATE: 2000-12-27
NUMBER OF SEQ 1D NOS: 4
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Best Local Similarity 99.6%; Pred. No. 5.3e-226;
Matches 466; Conservative 2; Mismatches 0;
Sequence 4, Application US/10028946; Patent No. 6734009; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: homo sapiens
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| Patent No. 6680188 | GENERAL INFORMATION:
| APPLICANT: WESSETER, Marion et al |
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND INTILE OF INVENTION: THEREOF |
| TITLE OF INVE
                                                                                                                300 TPFTEGTSARTFNNIMNPQRFLKFPDDPKVSSELLDLLQSLLCVQKERLKFEGLCCHPPF
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480 ILQSIYAEGSAGGHC 494
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Sequence 4, Application US/09804471A

Patent No. 6479269

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/804,471A

CURRENT APPLICATION NUMBER: 2001-03-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FRSESEQ for Windows Version 4.0
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                                                                                                                                                                                             93.8%; Score 2440; DB 4; Length 2054; 99.6%; Pred. No. 5.7e-226; ive 2; Mismatches 0; Indels 0
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  SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 2
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Matches 432; Conservative
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TYPE: PRT
ORGANISM: Mus Musculus
                                                                                TYPE: PRT
ORGANISM: homo sapiens
US-10-028-946-2
                                                                                                                                                                                                                          Similarity
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Best Local Simil
Matches 466; C
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US-09-804-471A-4
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US-09-804-471A-4
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US-09-916-204-4
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Sequence 2, Application US/09916204

Sequence 2, Application US/09916204

Sequence 2, Application US/09916204

Sequence 2, Application US/09916204

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

THEREOF INVENTION:

SOUTHWARE OF SEQ ID NOS:

SOUTHWARE:

SOUTHWARE FREESEQ FOR WINDOWS VERSION 4.0
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                                                               421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELODSQDKCHKVFISAAGLIPCSR 480
SPFAEGTSARTFINIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
                                                                                                            SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
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480 ILQSIYAEGSAGGHC 494
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Best Local Similarity 99.6
Matches 251; Conservative
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ORGANISM: Human
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US-10-282-048-2
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Sequence 2, Application US/10282048
Patent No. 6692948
GENERAL INFORMATION:
PAPLICANT: WEI, MING-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

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Sequence 4, Application US/09916204

Patent No. 6638745

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: AND USES
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45.3%; Score 1180; DB 4; Length 251;
Best Local Similarity 90.4%; Pred. No. 1.2e-105;
Matches 227; Conservative 13; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 257;
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Pred. No. 1.1e-115;
1; Mismatches 0;
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLOO1164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOCHWARE: PSELSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRI
; ORGANISM: Human
US-10-282-048-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.6%;
Matches 251; Conservative
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ORGANISM: Rattus norvegicus
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US-09-916-204-6
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US-10-282-048-5
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US-09-916-204-5
; Sequence 5. Application US/09916204
; Patent No. 663045
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NOS: 6
; SEQ ID NO 5
; TOWNEY OF SEQ ID NOS: 6
; TOWNEY OF SEQ
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Patent No. 6692948

GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: THEREOF
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Best Local Similarity 90.4%
Matches 227; Conservative
                                                                                                                                                                                                                                              241 GSAAKMINSNKV 251
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US-10-282-048-4
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RESULT 12
US-09-916-204-6
; Sequence 6, 38plication US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REPERENCE: C1001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 251
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  Length 251;
                                              Indels
Query Match
45.2%; Score 1177; DB 4;
Best Local Similarity 90.0%; Pred. No. 2.4e-105;
Matches 226; Conservative 16; Mismatches 9;
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       ECSOPALMKMKHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120
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                                                          239 EDGTVQSSVAVGTPDYISPEILQAME-DGKGRYGPECDWWSLGVCMYEMLYGETPFYAES
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358 DWDNIRNCEAPYIPEVSSPTDTSNFDVDDDCLKNSETMPPP---THTAFSGHHLPFVGFT
                                       121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG
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                                                                                                                          1 FKGKPAEIEANMSGEVRLRQLEQFILDGPAQTNGQC--FSVETLLDILLCLYDECNNSPL
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38.8%; Pred. No. 1.4e-77;
ive 93; Mismatches 145;
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Best Local Similarity 38.8%
Matches 187; Conservative
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US-09-949-016-8511
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Patent No. 6692948

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al.

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/10/282,048

CURRENT APPLICATION NUMBER: US/10/282,048

CURRENT FILING DATE: 2002-10-29

NUMBER OF SEQ ID NOS: 6

SOOFWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6
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Sequence 5, Application US/10282048
Patent No. 662948
GENERAL INFORMATION:
APPLICANT: WEL, MAING-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, ITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1164CIP-DIV
CURRENT APPLICATION NUMBER: US/10/282,048
CURRENT FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5.
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                                                                                                                                                                                                                                                                                                                Length 251;
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                                                                                                                                                                                                                                                                                                               45.2%; Score 1177; DB 4; 90.0%; Pred. No. 2.4e-105; tive 16; Mismatches 9;
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; ORGANISM: Mus musculus
US-10-282-048-6
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226; Conservat
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Best Local S
Matches 226
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063644 rattus norv
077819 o rho-assoc
028021 bos taurus
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Q9vty8 drosophila
Q01583 caenorhabdi
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Q6dt37 homo sapien
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Q6xuh8 homo sapien
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088938 mus musculu
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                                                                  March 18, 2005, 15:22:34; Search time 174 Seconds (without alignments) 1462.663 Million cell updates/sec
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                                                                                                                                         1 MLKFKYGARNPLDAGAAEPI..........CSRILPSVYAKGSARGRCWL 497
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Q9Y582 1
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Q99646 1
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Q86xx3
Q86xx3
Q8iwq7
Q8iwq7
Q7tt49
Q7tt50
P92199
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                       Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                   1612378 seqs, 512079187 residues
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ROC2 HUMAN
ROC1 HUMAN
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Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Result ģ ROC1_RAT ROC1_RABIT ROC2_BOVIN

Q6p5z6 homo sapien O44368 drosophila	Q9wlb0 drosophila P70336 mus musculu					Qygane gailus gail 000565 homo sapien		
Q6P5Z6 O44368	Q9W1B0 ROC2 MOUSE	DMK MOUSE ROCZ RAT	DMK HUMAN	090779	Q9VXE3	000565 000565	Q6D171	Q6L535
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857.5	857.5 853.5	847	822.5	809	808	763.5	763	732.5
33	3.4 3.5	36	38	40	41	4 4 2 6	44	42

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BASEP, 137151; IMAN.

GO; GO:0005622; C:intracellular; IEA.

BO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:Protein serine/theonine kinase activity; IEA.

GO; GO:0005634; F:Protein serine/theonine kinase activity; IEA.

GO; GO:0005634; F:Transferase regulatory/interacting protein. .; IEA.

BO; GO:0005403; F:Transferase activity; IEA.

GO; GO:0007422; P:intracellular signaling cascade; IEA.

GO; GO:0007422; P:intracellular signaling cascade; IEA.

GO; GO:0007422; P:intracellular signaling cascade; IEA.

BO; GO:0007423; P:Intracellular signaling cascade; IEA.

BO; GO:0007424; GO:000749; P:Intracellular signaling cascade; IEA.

BO; GO:0007424; GO:000479; DAG PE BIND DOM 1; 1.

BO; GO:0007424; P:Intracellular signaling cascade; IEA.

BO; GO:0006476; P:Intracellular signaling cascade; IEA.

BO; GO:0006476; F:Intracellular signaling cascade; IEA.

BO; GO:0006476; GO:00064; F:Intracellular signaling cascade; IIA.

BO; GO:0006476; GO:00064; F:Intracellular signaling cascade; IIA.

BO; GO:0006476; GO:00064; F:Intracellular signaling cascade; IIA.

BO; GO:0006476; F:Intracellular
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                       FROURINGE FROM N.A.

Huang C.Q., Wu S.L., Shan Y.X., Liu S., Xiao P.J.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to the SerThr protein kinase family.

-!- SIMILARITY: Contains 1 PH domain.

EMBL, AX227469; AAP13528_1; -.
                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                  PRT; 2027 AA
                                                                               Q86UQ9;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
                                                                                                                                                                               Rho/rac-interacting citron kinase
                                                     PRELIMINARY;
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RESULT 1
Q86UQ9
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us-10-724-594-2.rup

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Pfam; PF00433; Pkinase_C; 1
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                                                                                                                                                                  ECSOPALMKIKHVSNFVRKYSDTIAELOELOPSAKDFEVRSLVGCGHFAEVQVVREKATG
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                                                                                                                 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE
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                                                                                           Gaps
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 2027 AA; 231429 MW; 6B1D8C3F661F357B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Citron Rho-interacting kinase short form.
Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:Protein serine/threonine kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:00046740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001668; P:protein amino acid phosphorylation; IEA.
InterPro; IPR001009; Kinase like.
InterPro; IPR00019; Prot kinase.
InterPro; IPR0002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002291; Yrr_pkinase.
InterPro; IPR00249; Tyr_pkinase.
Pf00069; Pkinase; I.
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Mao Y., Xie Y., Wu Q.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AY209000; AAP43922.1; -.
HSSP; P05132; 1ATP.
                                                                                          0; Indels
                                                                 Length
                                                               Score 2440; DB 2;
Pred. No. 5.7e-153;
2; Mismatches 0;
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                                                                 93.8%;
                                                               Query Match
Best Local Similarity 99.6
Matches 466; Conservative
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-I. Biol. Chem. 273:29706-29711(1998).

-I. SIMILARITY: Belongs to the Ser/Thr protein kinase family. BRBL, AR068623; ARC72822.1; -. HSSP, P31751; IMRV. MGD; MGI:1051313; Cit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ECSQPALMKIKHVSNFVRXSDT1AELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GSAAKANSNKAVNAKLPIGTPDYMAPEVLTVANGDGKGTYGLDCDWWSVGVIAYEMIYGR
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Prodom; PD000001; Prot_KinaBe; 1.
SMART; SM00220; S.TKC; 1.
SWART; SM00133; S.TK.X; 1.
SWART; SM0019; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
ATP-Dinding; KinaBe; Berine/threonine-protein kinaBe; TransferaBe.
SEQUENCE 482 AA; 54353 MM; 4F02AF6A32C73BAE CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDILINE=99009084; PubMed=9792683; DOI=10.1074/jbc.273.45.29706; Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E. Dotto G.P.;
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                                                                                                                                                                                                                                                                                                                                              Query Match 93.2%; Score 2425; DB 2; Length 482; Best Local Similarity 98.9%; Pred. No. 9.2e-153; Matches 463; Conservative 3; Mismatches 2; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
NAM-201-interacting citron kinase short isoform.
Name-Cit; Synonyms-Ctik-sk;
Mus musculus (Mouse).
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RT Cotton rho-interacting kinase, a novel tissue-specific ser/thr kinase ricitron rho-interacting kinase, a novel tissue-specific ser/thr kinase accompassing the Rho-Rac-binding protein Citron.";

J. Biol. Chem. 273:29706-29711 (1998).

J. Biol. Chem. 273:29706-29711 (1998).

C. -- SIMILARITY: Contains 1 PH domain.

ENBL: AP086624; ARC72823.1; -- RAC72823.1; -- RAC728233.1; -- RAC728233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ECSQPALMKWKHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DIYAMKVMKKKALLAQEQVSFFEEENILSESTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG 180
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                                                                                                                     TISSUE=Spleen; MBDLINE=9909084; PubMed=9792683; DOI=10.1074/jbc.273.45.29706; Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E. Dotto G.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R SMART; SM00109; CT; 1.

R SMART; SM00109; CN1; 1.

R SMART; SM00123; PH; 1.

R SMART; SM00123; PH; 1.

R SMART; SM00123; FKC; 1.

R SMART; SM00123; STKX; 1.

R PROSITE; PS00409; DAG PE BIND DOM 1; 1.

R PROSITE; PS50003; PH DOMAIN; T.

R PROSITE; PS50011; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS01009; PROTEIN KINASE ATP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00130; C1_1; 1.
Pfam; PF00180; CNH; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00069; PKinase; 1.
Pfam; PF00433; PKinase C; 1.
PRINTS; PR00194; TROPOMYOSIN.
PRODOM; PD0000000; Prot_Kinase; 1.
                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGELPFVGFS 420
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GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR001009; Kinase like.

R InterPro; IPR001009; Kinase like.

R InterPro; IPR001009; Finase C.

R InterPro; IPR002719; Prot kinase.

R InterPro; IPR002719; For thr pkinase.

R InterPro; IPR001009; Finase; I.

R Pfan; PF000433; Pkinase; I.

R SMART; SM00133; Fixe; I.

R SMART; SM00133; G. TK X; I.

R PROSITE; PS00107; PROTEIN KINASE ATP; I.

R PROSITE; PS00119; PROTEIN KINASE DOM; I.

R PROSITE; PS00119; PROTEIN KINASE ST; I.

M ATP-binding; Kinase; Serine(threonine-protein kinase; Transferase.

SEQUENCE 494 AA; 55742 MW; 2C60D2294B2BA185 CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Last annotation update)
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87.3%; Score 2271.5; DB 2
Best Local Similarity 87.3%; Pred. No. 1.5e-142;
Matches 432; Conservative 27; Mismatches 35;
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Straubberg R.L., Feinged E.A., Grouse L.H., Derge J.G.,
Rausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan R.J., McKernan R.J., Marastne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Ratcheley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Renes S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                           241 GSAAKMISIKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
                      DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG
                                          241 GSAAKANSIK-VDAKLPIGTPDYMAPEVLTVANEDRRGTYGLDCDWWSVGVVAYEMLYGK
                                                                                                                                                                                                                                                                                                      360 ARTDWINIRNSPPPFVPTLKSDDDTSNFDEPERNSWWSSSPCQLSPSGEELPFVGFS
                                                                                                        DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                                                                                                                               301 SPFAEGTSARTFNNIMNFQRFLKPPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF
                                                                                                                                                                                                                                                                                                                                                                  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDBPBKNSWVSSSPCQLSPSGFSGEELPFVGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Medin S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; Romeric and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 YSKALGYLGRSESVVSGLDSPAKVSSMEK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 YSKALGILGRSESVVSGLDSPAKTSSMEK 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cdc42bpb protein (Fragment)
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QBAVMO;
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DFLSLLNRYEDQLDESMIQFYLAELILAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF 240
                                          GSAAKMISIKWVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
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                                                                GSAAKONSNK-VDAKLPIGTPDYMAPEVLTVONBEDRRGTYGLDCDWWSVGVVAYEMVYGK
                                                                                                                                                       TPFTEGTSARTFNNIMNFQRFLKFPDDPKVSSELLDLLQSLLCVQKERLKFEGLCCHPFF
                                                                                                                                                                                                                                            Later Discovery 1998;

Hash; AF070065; AAC27932.1;

Hash; AF070065; AAC27932.1;

Hash; AF070065; AAC27932.1;

R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R HoterPro; IPR00091; Pkinase_like.

R InterPro; IPR00019; Prot kinase.

R InterPro; IPR00019; Prot kinase.

R InterPro; IPR00019; Prot kinase.

R PRODON; PRO000001; Prot kinase.

R PRODON; PROCONON; Ser thr pkin_AS.

R PRODON; PROCONON; PROTEIN KINASE ATP; 1.

R PROSITE; PS00117; PROTEIN KINASE ATP; 1.

R PROSITE; PS00117; PROTEIN KINASE_DON; 1.

R PROSITE; PS00117; PROTEIN KINASE_DON; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                               SPFAEGTSARTFINIMINFORFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF
                                                                                                                                                                                                                 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGEELPFVGFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Citron-K kinase (Fragment).
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Madaule P., Eda M., Watanabe N., Fujisawa K., Matsuoka T., Bito H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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"Role of Citron kinase as a target of the small GTPase Rho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.9%; Score 2157.5; DB 2; Length 90.9%; Pred. No. 4.8e-135; ive 21; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                   YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV
                                                                                                                                                                                                                                                                                                                                         YSKALGYLGRSESVVSSLDSPAKVSSMEKKLLIKSKELQDSQDKCHKM
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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109 AEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKN 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 VDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 VGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLLCGQKE 347
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                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                             Ng Y. Tan I., Lim L., Leung T.;
Submitted (JUN-2004) to the EMEL/GenBank/DDBJ databases.

-1. SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-1. SIMILARITY: Conclains 1 PH domain.
EMBL, AY648038; AAT67172.1;
-2. GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:Protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein exina/threonine kinase activity; IEA.
GO; GO:0005242; F:manl GPase regulatory/interacting protein.
GO; GO:0005742; P:intracellular signaling cascade; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 35.7%; Score 929; DB 2; Length 1551; Similarity 43.8%; Pred. No. 8.2e-53; 34; Conservative 83; Mismatches 125; Indels 28
Myotonic dystrophy kinase-related CDC42-binding kinase gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001180; Citton.
InterPro; IPR001219; DAG PE-bind.
InterPro; IPR001209; Kinase like.
InterPro; IPR001009; Kinase like.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR001849; Prot kinase.
InterPro; IPR002190; Ser_thr.pkinase.
InterPro; IPR002290; Ser_thr.pkinase.
InterPro; IPR002290; Tor_kinase.
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 RFLKFPDD-PKVSSDFLDLIQSLLCGQKERLKFEGL---CCHPFFSKIDWNIRNSPPPF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 VPTLKSDDDTSNPDEPE---KNSWVSSSPCQLSPSGFSGEELPFVGFSYSK------ 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 IPDVSSPSDTSNFDVDDDILRNPEVIPSS---THSGFSGFHLPFVGFTYTTDSCFSDRGS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 RASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFV---RK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; PG015524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000674; F:protein serine/threonine kinase activity; IEA.

GO; GO:000674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006469; F:transferase activity; IEA.

GO; GO:0006469; F:protein amino acid phosphorylation; IEA.

InterPro; IPR0101909; Kinase Cilke.

R InterPro; IPR00051; Prot kinase.

R InterPro; IPR000590; Ser thr pkinase.

R InterPro; IPR00139; Prot kinase.

R Prodom; PO00001; Prot kinase; I.

R SWART; SM0013; FIX X; I.

R SWART; SM0013; STKX; I.

R PROSITE; PS01107; PROTEIN KINASE ATP; I.

R PROSITE; PS01107; PROTEIN KINASE DOM; I.

R PROSITE; PS0111; PROTEIN KINASE ST; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase, NON TRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ALGILGRSESVVSGLDSPAKTSSMEKKL-----LIKSKELQDS 461
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC041741; AAH41741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.7%; Score 929; DB 2; Length 717; 41.7%; Pred. No. 3.1e-53; Live 84; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     717 AA; 83371 MW; 2D295D4A8A5B733A CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 41.7%
Matches 196; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REDITINE-20196005; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hobskins R.A., Galle R.P., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hobskins R.A., Galle R.P., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., B. Stutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers R.A., M. H.J., Andrews-Pfeankoch C.R., Gabdwin D., R.A. Barl M.M. Baru A., Baxendale J., Bayraktaroll L., Baddwin D., Rallew R.W., Baruh A., Baxendale J., Bayraktaroll L., Beasley B.M., Beeson K.Y., Benco P.V., Berman B.P., Bhandari D., Bolchakov S., Borkova D., Botchan M.R., Bouck J., Bhandari D., Bolchakov S., Borkova D., Butler H., Cadieu E., Center A., Chadra I., Bartis R.C., Busam D.A., Dahlke C., Davemport L.B., Davies P., Bartis R.C., Busam D.A., Dahlke C., Perraz C., Perria C., Ferraz C., Perria C., Gabrielian A.E., Dondon K., Doup LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunkov G., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A Hostin D., Houston K.A., Mellan P., Karpen G.H., Re Z., Kemingon J.A., Ketchum K.A., Alush P., Karpen G.H., Re Z., Kemingon J.A., Ketchum K.A., Alush P., Karpen G.H., Re Z., Kemingon J.A., Ketchum K.A., Moy M., Moy M., Moy M., Moy M., Moy M., D., Noshrefia A., Moy M., Moy M., Moy M., Moy M., Moy M., Wixon K., Mussher D.B., Dacieler F., Shen H., Shue B.C., Siden-Kiamos I. Singson M., Strong N., Bacler K., Sandina M., Zhong P., Liu Y., Shen H., Spier B., Spradling A.C., Stapleton M., Strong N., Shoul B.C., Siden-Kiamos I. Singson M., Strong N., Woodager, Wolley M., Zhong W., Zhou G., Zhao Q., Zhao Q., Zhao Q., Zhao Y., Zhong W., Zhong W., Zhong W., Zhou S., Zhao G., Zhao G., Zhao 
                                                                                                                                                                                  457
                                                                                                                                                                                                                                425
RLKFEGL----CCHPFFSKIDWNNIRNSPPFFVPTLKSDDDTSNFDEPEKNSWVSSSPCQL 404
                                                                                                           379 PPPSHGAFSGHHLDFVGFTYT----SGSHSPESSSEAWAALERKLOCLEOE
                                                                                                                                                                             405 SP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTS----SMEKKLLIKSKE
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MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo!
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      PRT; 1854 AA
                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
CG10522-PA.
ORFNames=CG10522;
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Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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109 VTT 8
109 VTT 8
109 VTT 8
100 VTT 8
101 VT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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                                                                                                                                                                                                                                                                                                                                                                                                                               "The transposable elements of the Drosophila melanogaster euchromatin:
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Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=22426069; PubMed=12537572;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettenourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWART; SM00120; STRC; 1.

PROSITE; PS50081; DAG PE BIND DOM 2; 1.

PROSITE; PS50081; DAG PE BIND DOM 2; 1.

PROSITE; PS0107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 1854 AA; 211323 MW; 93E5B69FB63DEEID CRC64;
                                                                                                                                                                                                                                                                                   MEDLINE=22426070; PubMed=12537573;
Maninker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas
Patel S., Frise E., Wheeler D.A., Lewis S.B., Rubin G.M.,
Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AE003541; AAF49907.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                   melanogaster euchromatic genome sequence."
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InterPro; IPR001180; Citron.
InterPro; IPR001219; DaG_PB-bind.
InterPro; IPR001209; Kinase like.
InterPro; IPR000961; Pkinase C.
InterPro; IPR000961; Pkinase C.
InterPro; IPR000919; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
Pfam; PF00069; Pkinase; 1.
Pfam; PF00069; Pkinase; 1.
Pfam; PF00069; CII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0036295; CG10522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a genomics perspective.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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373 PEDTSNFDVDVCED--DFTPCLQETQPPRVLAAFTGNHLPFVGFSYTHG-SLLSDARSLT 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 AVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 VLTVWNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 P---KYSSDFLDLIQSLLCGQKERLKFEGLC---CHPFFSKIDWNIRNSPPFFVPTLKS 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 DDDTSNFDEPEKNSWVSSSPC--QLSP----SGFSGEELPFVGFSYSKALGILGRSESVV 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 NIYMDG-----PSKKKPEALSFETLIDSLICLYDECCNSTLRKEKCIAEFVESVKTVISKA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 ILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 EIDWVVSEEAKDLIRQLICSSDVRFGRNGLSDFQLHPFFEGIDWNTIRDSNPPYVPEVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 NLFFQGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase
                                                                               WormBase; WBGene00006437; K08B12.5.
WormBay; K08B12.5; CE30B18.
GO; GO:0005524; F:APP binding; IEA.
GO; GO:0005674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0005083; F:small GTPase regulatory/interacting protein. .
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SMOOLOG; LAGEBLOWAIN.

SMART; SMOOLOG; CNH; 1.

SMART; SMOOLOGS; PBD; 1.

SMART; SMOOLOGS; PBD; 1.

SMART; SMOOLOGS; PBD; 1.

SMART; SMOOLOGS; PBD; 1.

SMART; SMOOLOGS; PRC; 1.

SMART; SMOOLOG; STKC; 1.

SMART; SMOOLOG; PKC; 1.

SMART; SMOOLOG; PKC; 1.

SMART; SMOOLOG; PRC BIND DOM 1; 1.

PROSITE; PSSOOR; PAG PE BIND DOM 2; 1.

PROSITE; PSSOOR; PROTEIN KINASE ATP; 1.

PROSITE; PSSOOLOG; PROTEIN KINASE DOW; 1.

PROSITE; PSSOOLOG; PROTEIN KINASE DOW; 1.

PROSITE; PSSOOLOG; PROTEIN KINASE DOW; 1.

PROSITE; PSSOOLOG; PROTEIN KINASE STY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 34.5%; Score 897.5; DB 2; Best Local Similarity 40.5%; Pred. No. 1e-50; Matches 178; Conservative 91; Mismatches 150;
                                                                                                                                                                                                                           InterPro; IPR001180; Citron.
InterPro; IPR001219; DAG PR-bind.
InterPro; IPR001209; Kinase like.
InterPro; IPR001009; Kinase like.
InterPro; IPR001009; Rinase C.
InterPro; IPR001009; Phinase C.
InterPro; IPR0001919; Prot Kinase.
InterPro; IPR000219; Prot Kinase.
InterPro; IPR002209; Ser thr pkinase.
InterPro; IPR002209; Ser thr pkinase.
InterPro; IPR00130; Cl 1; 1.
Pfam; PF00130; CNH; 1.
Pfam; PF001431; Phinase C; 1.
Pfam; PF001431; Phinase C; 1.
-!- SIMILARITY: Contains 1 PH domain.
                      EMBL; U97001; AAB52260.3; -. PIR; T25808; T25808.
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                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                              : :|| :| : |||||: | | :||: || 361 VINPSKRLSYERIKNHPFFSEIPWGSIRSQVPPIIPTVRSDDDTSNFEDGIRHKTRREQG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVQVVREKATGDIYAMKVMKKKALLAQEQVSFPEEERNILSRSTSPWIPQLQYAFQDKNH 169
                                                                                                                                                                                                                                                                                                                                                           LCGQKERLKFEGLCCHPFFSKIDWNIRNSPPFVPTLKSDDDTSNFDE-----PEKN 394
                                       395 SWVSSSPCQLSPSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIK 454
                                                                                                                            LYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILV
                                                                                                                                                                                       DRTGHIKLVDFGSAAKMISNKMVNAKLPIGTPDYMAPEVLTVMNGD--GKGTYGLDCDWW
                                                                                                                                                                                                                                                                         SVGVIAYEMIYGRSPFAEGTSARTFNNIM-----NFQRFLKFPDDPKVSSDFLDLIQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda, Chromadorea, Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wormbase Consortium;
"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
Becker M., Wohldmann P.;
"The sequence of C. elegans cosmid KOBB12.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Temporarily assigned gene name protein 59.
Name=tag-59; ORFNames=K08B12.5;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Submitted (AUG-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKEL 458
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MALSON BELLES

MALSON BELLY, Belngold E.A., Grouse L.H., Derge J.G.,

MALSON BELLY, Colling F.S., Wagner L., Shanmen C.M., Schuler G.D.,

MALSCHUL S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

MALSCHUL S.F., Jordan H., Moore T., Max S.L., Rubin G.M., Hong L.,

Matchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Matchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Man S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Milalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Milalon D.K., Maray D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Modriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Mara M.J., Mara M.J.,

Mara M.J., Mara M.J.,

Machara M.J., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Generation and initial analysis of more than 15,000 full-length human
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R InterPro; IPR011009; Kinase like.
R InterPro; IPR000961; Prinase C.
R InterPro; IPR000290; Ser thr pkinase.
R InterPro; IPR000290; Ser thr pkinase.
R InterPro; IPR000290; Ser thr pkinase.
R Pfam; PF00069; Pkinase.
R Pfam; PF00063; Pkinase.
R Prodom; PR0013; Prot kinase.
R SMART; SM00120; Prot kinase.
R PROSITE; PS0010; PROTEIN KINASE ATP; 1.
R PROSITE; PS0010; PROTEIN KINASE ST; 1.
R PROSITE; PS0010; PROTEIN KINASE ST; 1.
R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56805 MW; 5F9FBD9CC1D2AEFC CRC64;
                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                              492 AA
                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                              PRT;
                                     430 DEIRAIAQRCQGDAELMEKS 449
436 SGLDSPAKTSSMEKKLLIKS
                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, CDC42BPB protein (Fragment). Name=CDC42BPB;
                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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Score 896.5; DB 2; Length 492; Pred. No. 2.8e-51;

34.5%;

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CTISSUE-Peripheral Nervous System;

XX TISSUE-Peripheral Nervous System;

XX TISSUE-Peripheral Nervous System;

XX Straubberg R.L., Felagold E.A., Grouse L.H., Derge J.G.,

XX Altausher R.D., Colling F.S., Margner L., Shenmen C.M., Schuler G.D.,

XX Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Halshe F.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Modin T.B., Toshiyuki S., Carninoi P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Raha S.S., Worden P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Richards S.W. Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XX Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XX Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XX Hilalon B., Ketteman M., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Hilalon M., Touchman J.W., Green B.D., Dickson M.C.,

XX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butrerfield Y.S.,

XX Green B.D., Marra M.A.,

XX Green S.J., Marra M.A.,

XX Green S.J.,

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                                                                44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
                                                                                                                                                                                                      104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYA 163
                                                                                                                                                                                                                                                                                                                                            164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PENILVDRTGHIKLVDFGSAAKMISNKWYNAKLPIGTPDYMAPEVLTWMGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEERFQFPSHVTDVSEEÄKDLIQRLI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :: || || : : || || 322 CSRERRIGGONGIEDFKKHAFFEGINWENIRNIEAPYIPDVSSPSDTSNFDVDDDVLRNTE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 CGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPE---KNSW 396
                                                                                                                                     82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 VSSSPCQLSP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI
29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
85; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 KSKELQDSQDKCHKVFISA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ::: | : | | : | | 426 KDEDVQ--RDLEHSLQMEA 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDC42BPB protein (Fragment)
Name=CDC42BPB;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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Service Services Serv

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143 FQDENHLYLVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99216425; PubMed=10198171; DOI=10.1006/geno.1999.5769;
Moncrieff C.L., Bailey M.E., Morrison N., Johnson K.J.;
"Cloning and chromosomal localization of human Cdc42-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Gaps
                                                                                                                                                                                                                                                                                                                                                                         R GO; GO: 0005856; C: cytoskeleton; TAS.

R GO; GO: 0005856; C: cytoskeleton; TAS.

R GO; GO: 0004672; F: protein kinase activity; TAS.

R GO; GO: 0007163; P: setablishment and/or maintenance of cell po. . .;

R GO; GO: 0007163; P: signal transduction; TAS.

R InterPro; IPR001180; Citron.

R InterPro; IPR001180; Citron.

R InterPro; IPR001180; Kinase like.

R InterPro; IPR001849; PH.

R InterPro; IPR001849; PH.

R InterPro; IPR00199; Kinase C.

R InterPro; IPR00199; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002291; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding, Kinase, Serine/threonine-protein kinase, Transferase
SEQUENCE 1711 AA, 194356 MW; 3A3731D40A363497 CRC64;
                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1711;
                                                                                                                                                                                                                                                                                 Genomics 57:297-300(1999).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family BMBL; AF128625; AAD37506.1; --
HSSP; P31751; 1MR.
                                         Query Match
34.5%; Score 896.5; DB 2; Length
Best Local Similarity 42.1%; Pred. No. 1.3e-50;
Matches 185; Conservative 85; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00479; DAG PE BIND DOM 1; 1.
PROSITE; PS50081; DAG PE BIND DOM 2; 1.
PROSITE; PS50003; PH DOMAIN; I.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ### PRO0130; C1 1; PERUSALIT, PERUF, PERUF, PERUF, PERUF, PERUF, PERUF, 1.

PERUF, PP00786; PBD; 1.

PERUF, PP00786; PBD; 1.

PERUF, PR00089; PKINASE; 1.

PEDDON; PD000001; PEDC_KINASE; 1.

SWART; SM00109; C1; 1.

SWART; SM00285; PBD; 1.

SWART; SM00231; PH; 1.

SWART; SM00213; PH; 1.
                          Homo sapiens (Human)
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                   TISSUE=Brain;
       원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PODKOWILYLVMEYOPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEERFQFPSHVTDVSEEAKDLIQRLI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGOKERLKFEGL---CCHPFFSKIDWNNIRNSPPFFVPTLKSDDDTSNFDEPE---KNSW 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 I-----LPPGSHTGFSGLHLPFIGFTFT-----TESCFS--DRGSLKSIMOSNTLT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 VSSSPCQLSP---SGPSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 SALSVETLEDVLVCLYTECSHSALRRDKYVAEFLEWAKPFTQLVKEMQLHREDFEIIKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                              Definition (TMAK-2003) to the Employermous, burden delanger of the State of the Ser/Thr protein kinase family.

EMBL; BC047871; AM447871.1; ---

EMBL; BC047871; AM447871.1; ---

EMBL; BC047871; IMAY.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0016740; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0016740; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0016719; F:protein serinese.

InterPro; IPR000951; Prinase Iike.

InterPro; IPR000951; Prinase Iike.

InterPro; IPR000951; Prinase; I.

R Fam; PF000063; Prinase; I.

R Frodom; PF0000061; Protein kinase; I.

R SWART; SW00133; FIK x; I.

R SWART; SW00133; FIK x; I.

R ROSITE; PS00101; PROTEIN KINASE DOM; I.

R PROSITE; PS00108; PROTEIN KINASE DOM; I.

R PROSITE; PS00108; PROTEIN KINASE DOM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.5%; Score 896.5; DB 2; Length 933; 42.1%; Pred. No. 6.2e-51; tive 85; Mismatches 140; Indels 29
SEQUENCE FROM N.A.
TISSUE=Peripheral Nervous System;
Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ dàtabases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    933 AA; 108543 MW; 38E7179C3253F521 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CDC42-binding protein kinase beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 KSKELQDSQDKCHKVFISA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 42.1.
Matches 185; Conservative
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SEQUENCE
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09Y5S2
1D 09Y5S:
AC 09Y5S:
DT 01-NO
DT 01-MA
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496 AA
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Q99646
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CGOKERLKFEGL---CCHPFFSKIDWNNIRNSPPFFVPTLKSDDDTSNFDEPE---KONSW 396
                                                                                                                         397 VSSSPCQLSP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Brain,

X TISSUB-Brain,

X TISSUB-Brain,

X Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;

A Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;

A Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;

XI "Characterization of cDNA clones selected by the Genemark analysis

XI "Characterization of cDNA libraries from human brain.";

IN RESP. PAINTIANITY: Belongs to the Ser/Thr protein kinase family.

C -!- SIMILANITY: Belongs to the Ser/Thr protein kinase family.

C -!- SIMILANITY: Contains 1 PH domain.

DR Resp. PAINTIA: IMRY.

EMBL; AB012950, BAA86438.2; -.

R HSSP; PAINTIA: IMRY.

R GG-10000524; F:ATC the Serine/threonine kinase activity; IEA.

GG GO:0000524; F:ATC the serine/threonine kinase activity; IEA.

GG GO:000542; F:ATC the serine/threonine kinase activity; IEA.

GG GO:000543; F:ATC the serine/threonine kinase activity; IEA.

GG GO:000543; F:ATC the serine/threonine kinase activity; IEA.

GG GO:000544; F:Protein amino acid phosphorylation; IEA.

B GG GO:000542; P:ATT analferse rightliar signaling cascade; IEA.

GG GO:000542; P:ATT analferse IIA.

GG GO:000542; P:ATT analferse IIA.

R GG GO:000542; P:ATT analferse IIA.

R GG GO:000543; F:ATT analferse IIA.

R GG GO:000544; F:PRO0189; F:ATT and IIA.

R INCEPPRO: IPR00189; F:ATT analferse IIA.

R INCEPPRO: IPR00189; PH.

R INCEPPRO: IPR000951; Protein amino acid phosphorylation; IEA.

R INCEPPRO: IPR000951; Proteinse C.

R INCEPPRO: IPR000951; Proteinse C.

R INCEPPRO: IPR000951; Sertir pkinase.

R INCEPPRO: IPR000951; Sertir pkinase.

R Pfam: PPRO/380: CI-1; I.

R Pfam: PPRO/380: CI-1; I.

R Pfam: PR00/380: CI-1; I.

R Pfam: PFR00180; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAA1124 protein (Fragment).
Name-KIAA1124,
Home saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1760 AA.
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SWART; SW00109; C1; 1.
SWART; SW00036; CNH; 1.
SWART; SW0028; PBD; 1.
SWART; SW00233; PH; 1.
SWART; SW00233; PH; 1.
SWART; SW00133; PH; 1.
PROSITE; PSS0108; CREB; 1.
PROSITE; PSS0108; CREB; 1.
                                                                                                                                                                                                                                                                                                                       454 KSKELQDSQDKCHKVFISA 472
                                                                                                                                                                                                                                                                                                                                                     | :::| :| KDEDVQ--RDLEHSLOMEA 442
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Pfam, PF00433; Pkinase C, 1.
PRINTS; PR00008; DAGPEDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Pfam; PF00786; PBD; 1
Pfam; PF00169; PH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Q9ULUS
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44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 PENILVORIGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :: | | | | : | | 371 CSRERRIGQNGIEDFKKKHAFFEGLNWENIRNLEAPYIPDVSSPSDTSNFDVDDVLRNTE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYA
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                                                                                                                                                                                                                                                                                                                                                                                 29; Gaps
PROSITE; PS50081; DAG PE BIND DOM 2; 1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
NON TER.
SEQÜENCE 1760 AA; 199208 WW; 3AICA9A7ABFSFA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO: GO:0004674; F:protein serine/threonine kinase activity; TAS. GO:0006468; P:protein amino acid phosphorylation; TAS. Interpro; IPR0011009; Kinase_like.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000719; Prot kinase.
InterPro; IPR0002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                              Length 1760;
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Zhao Y., Kidd V., Kraft A.S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; US9305; AAB37126.1; -.
HSSP; P31751; 1MRY.
                                                                                                                                                                                                                                                                                                   Query Match

34.5%; Score 896.5; DB 2; Length
Best Local Similarity 42.1%; Pred. No. 1.4e-50;
Matches 185; Conservative 85; Mismatches 140; Indels
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01-MXY-1997 (TrEMBLrel. 03, Last sequence update)
01-MXY-1997 (TrEMBLrel. 25, Last annotation update)
Ser-thr protein kinase PK428.
Homo sapiens (Human).
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F:small GTPase regulatory/interacting protein.
                                                                                              InterPro; IPR001180; Citton.
InterPro; IPR001219; DAG PE-bind.
InterPro; IPR001009; Kināse like.
InterPro; IPR001009; Kināse like.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR000719; Prot kināse.
InterPro; IPR000719; Prot kināse.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfām; PP00180; Cl. 1; 1.
Pfām; PP00169; PH; 1.
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423 KQRLSPDSTRKLQD 436
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Best Local Similarity 41.0
Matches 178; Conservative
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Job time : 179
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYVHRDIKPENILVDRTGHIKLVDFGSAAKMISNKMVNAKLPIGTPDYMAPEVLTVMNGD 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDLIQSLLCGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPFVPTLKSDDDTSNFDEP 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 KOLIRRLICSREHRLGQNGIEDFKKHPFFSGIDWDNIRNCEAPYIPEVSSPTDTSNFDVD 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDCLKNSETMPPP---THTAFSGHHLPFVGFTYTSSCVLSDRSCLRVTAGPTSLDLDVNV 431
                                                                                                                                                                                                                                                                                                                                                                                           75
                                                                                                                                                                                                                                                                                                                                            36 PPWTQQQMSPLSREGILDALFVLPBECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAK 95
                                                                                                                                                                                                                                                                                                                                                                          PAQTNGQY--FSVETLLDILICLYDECNNSPLRREKNILEYLEWAKPFTSKVKQMRLHRE
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
Pfam; PP00433; Pkinase C; 1.

ProDom; PD00001; Prot_kinase; 1.

SMART; SM00220; 2.TKc; 1.

SMART; SM00137; 5.TKc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serime/threonine-protein kinase; Transferase.

SEQUENCE 496 AA; 56991 MW; 069186D74AE9C936 CRC64;
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EMBL, AAABO1008986; EAAO1280.2; -.

HSSP; P31751; IMRV.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
                                                                                                                                                                                                                                                                                                  34;
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
--- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                Length 496;
                                                                                                                                                                                                                                              34.2%; Score 891; DB 2; Length 496
40.3%; Pred. No. 6.5e-51;
tive 92; Mismatches 145; Indels
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Last annotation update)
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432 QRTLDNNLATEAYERRIKRLEQEKLELSRKLQES 465
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Q7PV87;
Q7PV87;
Q7MR7-2004 (TrEMBLrel. 26, Cre 01-MAR-2004 (TrEMBLrel. 26, Las 01-MAR-2004 (TrEMBLrel. 26, Las ENSANGP0000009214 (Fragment).
                                                                                                                                                                                                                                                                       Best Local Similarity 40.3%
Matches 183; Conservative
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20 ;
      GO; GO:0005083; P:small GTPase regulatory/interacting prot
60; GO:0016740; P:transferase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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Pfam, PP00169; PK: Description of PP00169; PK: Description of PP00169; PK: Description of Pr00169; PK: Description of Pr00169; PR001718; PS010001; Pr00169; PR001718; PS01019; PR001718; PS01019; PR001718; PS01019; PR001718; PS01019; PR001718; PS01019; PR001718; PS01019; PR001719; PR001718; PS01019; PR001719; PR001719; PR001718; PS01019; PR001719; PR0017
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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 18, 2005, 15:30:56; Search time 42 Seconds (without alignments) 1138.565 Million cell updates/sec Run on:

Title: Perfect score:

US-10-724-594-2 2602 1 MLKFKYGARNPLDAGAAEPI......CSRILPSVYAKGSARGRCWL

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

372

328 P---KVSSDFLDLIQSLLCGQKERLKFEGLC---CHPFFSKIDWNNIRNSPPFFVPTLKS 381

382 DDDTSNFDEPEKNSWVSSSPCQLSP----SGFSGEELPFVGFSYSKALGILGRSESVVSG 437

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serine/threonine k	probable protein k	hypothetical prote	myotonic dystrophy	tumor suppressor p	probable serine/th	probable serine-th	protein kinase DBF	protein kinase DBF	probable protein k	protein F27F5.23 [hypothetical prote	protein kinase (EC	probable serine/th	protein kinase (EC	probable prolifera
T47255	S22711	T25035	178395	A56155	S62556	T41341	859776	S64387	S22258	H96509	S63378	S41099	T38171	T17287	T50414
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480	620	906	412	1099	607	624	564	572	726	1092	893	425	646	462	269
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A,Residues: 1-1702 <LEU>
A,Rossi-references: UNIPROT:054875; EMBL:AF021936; NID:g2736152; PID:g2736153; PIDN:AACO:
A,Experimental source: brain
C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 PDNVLLDVNGHIRLADFGSCLKANDDGTVOSSVAVGTPDYISPEILQAME-DGMGKYGPE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 .CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEERFQFPSHVTDVSEEAKDLIQRLI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 CGOKERLKFEGL---CCHPFFSKIDMNNIRNSPPFVPTLKSDDDTSNFDEPE---KNSW 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :: | | | : : | | 322 CSRERRIGONGIEDFKKHAFFEGLNWENIRNLEAPYIPDVSSPSDTSNFDVDDDVLRNIE 381
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C;Species: Caenorhabditís elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 VSSSPCQLSP---SGFSGEELPFVGFSYS------KAL---GILGRSESVVSGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 I-----LPPGSHTGFSGLHLPFIGFTFTTESCFSDRGSLXSMIQSNTLTXDEDVQRDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 SSLSVETLLDVLVCLYTECSHSALRRDKYVAEFLEWAKPFTQLVKDMQLHREDFEIIKVI
                                                                 kinase acts as
                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1027-1076/Domain: protein kinase C zinc-binding repeat homology <KZN>
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     R;Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L. Mol. Cell. Biol. 18, 130-140, 1998
Mol. Cell. Biol. 18, 130-140, 1998
A;Reference number: 217862; MUID:98078670; PMID:9418861
A;Recession: T14050
A;Reterence number: translated from GB/EMBL/DDBJ
A;Recession: T14050
A;Returs: precliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.5%; Pred. No. 3.2. tive 90; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.9%; Score 883; DB 2; 40.5%; Pred. No. 3.4e-32;
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C;Keywords: ATP; phosphotransferase
F;74-342/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 SPAKTSSMEKKL-----LIKSKELQDS
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R;Dante, M.; Wamsley, P.
submitted to the EMBL Data Library,
A;Description: The sequence of C. el
A;Reference number: Z20047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 40.5%
Matches 182; Conservative
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A;Gene: CESP:C10H11.9
A;Map position: 1
                                                                                                                                                                                                                                                                                                                          A; Gene: MRCK-beta
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                                                                                                                                                                                                                                                         protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - rat C;Species: Ratus norvegicus (Norway rat) C;Becies: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004 C;Bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004 C;Bccession: T14039 F;Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L. Mol. Cell. Biol. 18, 130-140, 1998 A;Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector A;Reference number: Z17862; MUID:98078670; PMID:9418861 A;Accession: T14039 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1732 <LEU>A;Molecule type: mRNA A;Residues: 1-1732 <LEU>A;CGCONETION: A;CCONETION: A;CCONETION: A;CCOSETION: A;CCOSETION: A;CCOSETION: A;CCOSETION: A;CCOSETION: A;CCONETION: A;CCOSETION: A;CCOSETIO
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PEDTSNFDVDVCED--DFTPCETQPPRVLAAFTGNHLDFVGFSYTHG-SLLSDARSLTDE 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIPQLQYAFQDKWHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLM 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E---KNSWVSSSPCQLSPSGFSGEELPFVGFSYSKALGILGRS------ESV 434
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004
C;Accession: T14050
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K,Reywords: ATP; phosphotransferase
F;75-343/Domain: protein kinase homology «KIN»
F;1013-1062/Domain: protein kinase C zinc-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 891; DB 2; Length 1732; 40.3%; Pred. No. 1.5e-32; ive 91; Mismatches 146; Indels 3.
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                                                                                      LDSPAKTSSMEKKLLIKS
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Matches 183; Conservative
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C;Accession: S69211; S71910
R;Ishlizaki, T.; Mackawa, M.; Fujisawa, K.; Okawa, K.; Iwamatsu, A.; Fujita, A.; Watanabe EMBO J. 15, 1885-1893, 1996
A;Title: The small GTP-binding protein Rho binds to and activates a 160 kDa Ser/Thr prot A;Reference number: S69211; MUID:96203110; PMID:8617235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: 569211
A; Status: nucleic acid sequence not shown
A; Molecule type: many
A; Mesidues: 1.1354 <1SH1>
A; Residues: 1.1354 <1SH1>
A; Accession: $71910
A; Mesidues: 187-195; 281-288; 465-473; 573-587; 818-828; 885-893; 934-945 <1SH2>
C; Superfamily: protein kinase C zinc-binding repeat homology; protein kinase homology C; Keywords: APP: phosphotransferase; serine/threonine-specific protein kinase F; 74-338/Domain: protein kinase ATP-binding motif
F; 74-338/Domain: protein kinase ATP-binding motif
F; 1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>
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        CDWWSVGVFLYEMLVGDTPFYADSLVGTYSKIMNHKNSLTFPDDNDISKEAKNLICAFLT 318
                                                                                                                                                                                                                                                                                                                         319 DREVRIGERIGYEEIKRHLEPKNDQWAMETLRDTVAPVVAPDLSSDIDTSNFDDLEEDKGDE 378
                                                                                                                                                                                                                                                                             344 GOKERLKFEG---LCCHPFFSKID--WNNIRNSPPFFVPTLKSDDDTSNFDEPEKNSWVS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                     SS-PCQLSPSGFSGEELPFVGFSY----SKALGILGRSESVV--SGLDSPAKTSSME 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - human C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Aug-2004
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C; Species: Mus musculus (house mouse)
C; Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C; Accession: S74244
R; Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A; Title: ROCK-II, two isoforms of Rho-associated coiled-coil forming protein A; Reference number: S74244 MUID:96368048; PMID:8772201
A; Reference number: S74244
A; Residues: 1-1354 «NAk.>
A; Residues: 1-1354 «NAk.>
A; Residues: 1-1354 «NAk.>
A; Residues: UNIPROT: P70335; EMBL:U58512; NID:g1514695; PIDN:AAC53132.1; PID:g151C; Superfamily: protein kinase homology (C; Superfamily: protein kinase homology «KIN.>
F; 74-338/Domain: protein kinase homology «KIN.>
F; 72-9-1283/Domain: protein kinase C zinc-binding repeat homology «KZN.>
A;Introns: 23/3; 51/1; 104/3; 343/1; 478/2; 868/3; 891/3; 970/3; 1027/3; 1114/1
C;Superfamily: hypothetical protein C10H11.9; protein kinase homology
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                                                                                                                    DB 2; Length 1173;
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                                                                                                                Query Match 33.7%; Score 876.5; DB 2; Best Local Similarity 40.9%; Pred. No. 4.7e-32; Matches 168; Conservative 88; Mismatches 142;
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Schools and the contine specific protein kinase (EC 2.7.1.-), Rho-associated - bovine (Species Bordingenius taurus (cattle) (Species Bos primigenius taurus (cattle) (Cattl
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           344 GQKERLKFEG---LCCHPFFSKIDWNNIRNSPPFFVPTLKSDDDTSNFDEPEKNSWVSSS 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 YSKIMDHKNSLCPPEDAEISKHAKNLICAFLTDREVRLGRNGVEEIKQHPFFKNDQWNWD 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIRNSPPPFVPTLKSDDDTSNFDEPEKNSW-VSSSPCQLSPSGFSGEELPFVGFSYSKAL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
                                                                                                                                                                                                                                                                                                                      ::| | | ::
LSDIREGAPLGVHLPFVGYSYS----CMALRDSEVPG---PTPMEVEAEQLLEPHVQAPS
                                                                                                                                                                                               320 PPETRLGRGGAGDFRTHPFFFGLDWDGLRDSVPPFTPDFEGATDTCNFDLVEDGLTAMET
                                                                                                                                                                                                                                                                    401 PCOLSPSGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKIL---IKSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 ALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 VNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 FNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEG---LCCHPFFSKIDWN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAEPIAN----RASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIK
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                                                                                                                                                                                                                                                                                                                                                                                                                 LODS---ODKCHKVFISAA 473
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LEPSVSPQDETAEVAVPAA 451
                                                                                                                                                                                                                                                                                                                                                                                                                     458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1.417, 'L', 419-468, 'P', 470-544, 'MARRPWLWASARWWGQAPCTAATCCSLPGS', 'LGLAYRRRFPCS
A; Cross-references: GB:S72883; NID:g633864; PIDN:AAB31800.1; PID:g633865
A; Cross-references: GB:S72883; NID:g633864; PIDN:AAB31800.1; PID:g633865
A; Cross-references: GB:S72883; NID:g1863864; PIDN:AAB31800.1; PID:g18675; Call 68, 799-808, 1992
A; Parcol 1992
A; Parcol 1992
A; Parcol 1992
A; Release the munder: A42101; MUID:92154692; PMID:1310900
A; Receince number: A42101; MUID:92154692; PMID:1310900
A; Residues: 'PPGQVRGRLAVGGA', 57-550, 'WLWASARWWGQA', 564-624 <br/>A; Residues: 'PPGQVRGRLANGGA', 57-550, 'WLWASARWWGQA', SAGA', 57-550, 'WLWASARWGQA', SAGA', 57-550, 'WLWASARWGGA', 57-550, 'WLWASARWGGA', SAGA', 57-550, 'WLWASARWGGA', 564-624 <br/>A; Residues: 'PPGQWGA', S
                                                                                                                                                                                                                                                                                   RESULT 7
B49364
protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - human
N;Alternate names: myotonin protein kinase
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 16-Aug-2004
C;Accession: B49364, S48681; Ā42101
R;Shaw, D.J.; McCurrach, M.; Rundle, S.A.; Harley, H.G.; Crow, S.R.; Sohn, R.; Thirion, Genomics 18, 673-679, 1993
A;Title: Genomic organization and transcriptional units at the myotonic dystrophy locus.
A;Reference number: A49364; MUID:94140369; PMID:7905855
A;Accession: B49364
A;Residues: 1-624 eSHA>
A;Residues: 1-624 eSHA>
A;Residues: 1-624 eSHA>
A;Cross-references: UNIPROT:Q09013; GB:L19268; NID:g307176; PIDN:AAA36206.1; PID:g307177
R;Sassagawa, N.; Sorimachi, H.; Maruyama, K.; Arahata, K.; Ishiura, S.; Suzuki, K.
FEBS Lett. 351, 22-26, 1994
A;Title: Expression of a novel human myotonin protein kinase (MtPK) cDNA clone which enc
379 ETFPI---PKAFVGNQLPFVGFTYYSNRRYLSSANPNDNRTSSNADKSLQESLQKTIYKL 435
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Pred, No. 1e-31;
                                                                                                                  KE-----LQDS-QDKC 465
                                                                                                                                                            : | | : | | : | | EEQLHNEMQLKDEMEQKC 453
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Best Local Similarity 40.8 Matches 179; Conservative
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probable protein kinase YNL161w (EC 2.7.1..) - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypotherical protein N1727
C;Species: Saccharomyces cerevisian
C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 16-Aug-2004
C;Accession: S60966; S63113; S63813
R;Masr, F; Becam, A.M.; Herbert, C.J.
C,Accession: Sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 company obscription: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the left arm of chromosome XIV reveals 28 company of the sequence of 36.8 kb from the sequence of 
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A;Residues: 1-756 <NAS>
A;Residues: 1-756 <NAS>
A;Residues: 1-756 <NAS>
A;Cross-references: UNIPROT:P53894; EMBL:X92517; NID:g1050783; PIDN:CAA63278.1; PID:g105(R);Nasr, F; Becam, A.M.; Herbert, C.
B;Nasr, E; Becam, A.M.; Herbert, C.
A;Reference number: S62967
A;Reference number: S62967
A;Residues: 1-756 <NAW>
A;Ribast: 1-756 <NAW A:Herbert, C.J.
A;Residues: 1-756 <NAW A:Herbert, C.J.
A;Ribast: 1-756 <NAW A:Herbert, C.J.
A;Ribast: 1-756 <NAW A:Herbert, C.J.
A;Title: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 complete
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                                                                                                                                                                                                                                                                                336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 ADNSSQSTSKAGPWRKMLSSKDLNFVGYTY-KNPEIV--NDYQVPGIAELKKKDTKPKRP 428
                                                          276
                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                                      337 LIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEK 393
                                                                                                                                                                                                                                                                                                                                                                                                                                          312 LISKLLCNVTQRLGSNGAHEIKLHPWFNGIDWERIYQMEAAFIPEVNDELDTQNFEKFEE 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 NSWVSSSPCQLSP--SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKL 451
                                                                                                                                                                                                                                                                                                                252 KKGYGMECDWWSLGAIMYEMLVGYPPFYSDDPMSTCRKIVNWRTHLKFPEEAKLSPEAKD
                                                                                                                                                      ------SNKMVNAKLPIGTPDYMAPEVLTVMNGDG
                                                                                                                                                                                                              198 FEVNNGNGGSPSNEGSTKPRRIQQEQLQHWQKNRRMLAYSTVGTPDY1APEVLL----
                                                                                                                                                                                                                                                                            KGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFORFLKPPDDPKVSSDFLD
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                                196 NLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 756;
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A.Accession: S63813
A.Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.1%; Score 704; DB 2; L 32.7%; Pred. No. 1.4e-24; ive 82; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;350-672/Domain: procein kinase homology <KIN>F;358-366/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGD:S0005105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 LIKSKELQDSQD 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 SIKSLFEDESSD 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tonic dystrophy kinase.
A;Reference number: S60958
A;Accession: S60966
A;Molecule type: DNA
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A; Note: YNL161w
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C;Superfamily: Arabidopsis thaliana protein kinase T518.9; protein kinase homology
C;Keywords: ATP; phosphotransferase; protein kinase
F;38-338/Domain: protein kinase homology <LIN:
F;46-54/Region: protein kinase ATP-binding motif
                             A,Cross-references: UNIPROT:095A79; GB:AE005172; NID:g4587520; PIDN:AAD25751.1; GSPDB:GR
C,Genetics:
A,Map position: 1
C,Superfamily: Arabidopsis thaliana protein kinase T518.9; protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein kinase (EC 2.7.1.-) - common ice plant (fragment)
C;Species: Wesembryanthemum crystallinum (common ice plant)
C;Date: 06-Jan-1995 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: S42864
R;Baur, B.; Winter, K.; Fischer, K.; Dietz, K.
submitted to the EMBL Data Library, March 1994
A;Bescription: Molecular cloning and characterization of several protein kinases from A;Reference number: S42864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELDTQNPEKFDE----VPSTCQTSSKSSPWRKMISSKDANFLGYTF-KNLEIV--DEHHI 497
                                                                                                                                                                                                                                                                                                                    KIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVM 128
                                                                                                                                                                                                                                                                                                                                                                                                                                          KKKALLAQEQVSFFEBERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 KNFPDFKAELVDRSTKPAAEHDRLSKPPSAPRRTQQEQLLHWQQNRRTLAFSTVGTPDYI 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||||
331 APEVLL-----KKGYGMECDWWSLGAIMPEMLVGFPPFYSEEPLATCRKIVNWKTCLKF 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDDTSNFDEPEKNSWVSSSPCQLSPSG-----FSGEELPFVGFSYSKALGILGRSESVV 435
                                                                                                                                                                                                                                                                                                                                                        --NKMVNAKLPIGTPDYM 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDDPKVSSDFLDLIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPFFVPTLKS 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78
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                                                                                                                                                                                                                                                     68;
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                                                                                                                                                                                          Length 522;
                                                                                                                                                                                       Query Match 27.7%; Score 721; DB 2; Length 52 Best Local Similarity 35.9%; Pred. No. 1.8e-25; Matches 158; Conservative 82; Mismatches 132; Indels
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159; Conservative 7
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A,Molecule type: mRNA
A,Residues: 1-479 <BAU>
      <STO
A;Residues: 1-522
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C.E.; gene.

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Cispecies: Arabidopsis thaliana (mouse-ear crees)
Cispecies: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Atthores: Salzberg, S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Atthore: Sequence and analysis of chromosome of the plant Arabidopsis.
A;Title: Sequence and analysis of chromosome of the plant Arabidopsis.
                                                                                                                                                                                                                           46 LSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 DWWALGVFAYEMPYGQTPFYADSTAETYAKIVHYREHLSLPLADTVVPEEAQDLIRGLLC 319
                                                                             A;Cross-references: UNIPROT:P54265; EMBL:221505
R;Mahadevan, M.S.; Amemiya, C.; Jansen, G.; Sabourin, L.; Baird, S.; Neville,
Hum. Mol. Genet. 2, 299-304, 1993
A;Title: Structure and genomic sequence of the myotonic dystrophy (DM kinase)
A;Reference number: S38815; MUID:93271990; PMID:8499920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 GQKERLKFEG---LCCHPFFSKIDWNNIRNSPPFVPTLKSDDDTSNFD--EPEKNSWVS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 GAFSEVAVVKNKQTGQVYAMKIMNKWDMLKRGEVSCFREERDVLVKGDRRWITQLHFAFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKNHLYLVWEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 NILLDRCGHIRLADFGSCLKLQPDGMVRSLVAVGTPDYLSPEILQAVGGGPGAGSYGPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 LGLEPLLDLLLGVHQELGASHLAQDKYVADFLQWVEPIAARLKEVRLQRDDFEILKVIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NILVDRTGHIKLVDFGSAAKMISNKMVNAKLPIGTPDYMAPEVL-TVMNGDGKGTYGLDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFP-DDPKVSSDFLDLIQSLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 PAEIRLGRGGAGDFOKHPFFFFGLDWEGLRDSVPPFTPDFEGATDTCNFDVVEDRLTAMVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.6%; Score 847; DB 2; L
Best Local Similarity 44.3%; Pred. No. 4.7e-31;
Matches 171; Conservative 75; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase TSI8.9 protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                           C'Superfamily: protein kinase homology
C'Keywords: ATP; phosphotransferaes; protein kinase
F;69-339/Domain: protein kinase homology «KIN»
F;77-85/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 SSPCQLSPSGFS---GEELPFVGFSY 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 GGGETLSDMQEDMPLGVRLPFVGYSY 405
                                                       A; Residues: 1-557 < MAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: G86431
A;Status: preliminary
A;Molecule type: DNA
                                 A, Molecule type: DNA
                                                                                                                                                                                                                     A; Accession: S38815
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                                                                                                                                                                           Scrine/threonine-specific protein kinase (BC 2.7.1.-) isoform II, Rho-associated - mouse C;Species: Mus musculus (house mouse)
C;Species: Wus musculus (house mouse)
C;Date: 29-dan-1998 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C;Accession: S74245
R;Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A;Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A;Reference number: S74244; MUID:96368048; PMID:8772201
A;Accession: S74245
A;Cession: S74245
A;Cession: S74245
A;Cession: S74245
A;Cession: S74245
A;Cession: S74245
C;Cession: S74245
A;Cross-references: UNIPROT:P70336; EMBL:U58513; NID:g1514697; PIDN:AAC53133.1; PID:g151
C;Superfamily: protein kinase C zinc-binding repeat homology; protein kinase homology
C;Keywords: phosphotransferase; serinc-binding repeat homology <KEN>
F;1261-1315/Domain: protein kinase C zinc-binding repeat homology <KEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine/threonine-specific protein kinase (EC 2.7.1..) - mouse
NyAlternate names: myotonic dystrophy-associated protein kinase; myotonin protein kinase
C;Species Mus musculus (house mouse)
C;Date: 06-Dec-1996 #sequence revision 06-Dec-1996 #text_change 16-Aug-2004
C;Accession: S71829; S38815
C;Accession: S71829; S38815
S;Ambadevan, M.S.; Amemiya, C.; Jansen, G.; Sabourin, L.; Baird, S.; Neville, C.E.; Worm submitted to the EMBL Data library, January 1993
A;Description: Structure and genomic sequence of the myotonic dystrophy kinase (DM kinase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.8%; Score 853.5; DB 2; Length 1
40.0%; Pred. No. 5.7e-31;
cive 95; Mismatches 144; Indels
GILGRSESVVSGLDSPA--KTSSMEKKLLIKSKELQDSQDKCH 466
                                 NDAIQTR---KSEESQEIQKKLY 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 TSSMEKKLLIKSKELQDSQDKCH 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.8%
Best Local Similarity 40.0%
Matches 177; Conservative
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serine/threonine-specific protein kinase (EC 2.7.1.-) orb6 - fission yeast (Schizosacchan
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rosedidues: 1-469 <RIE>
A;Rosedidues: 1-469 <RIE>
A;Croserimental: Surces: UNIEROT: 013310; EMBL:AL121770; PIDN:CAB57446.1; GSPDB:GN00066; SPDB:&A;Experimental: Surces: Strain: 972h-; cosmid c821
B;Verde, F;, Wiley, D.J.; Nursee, P. Pz-6-7531, 1998
A;Title: Fission yeast orb6, a ser/thr protein kinase related to mammalian rho kinase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: coordinates maintenance of cell polarity during interphase with the c
A;Note: interacts genetically with orb2, which encodes the Pakl/Shk1 protein kinase
C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase
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A;Reference number: Z22544; MUID:98301608; PMID:9636183
A;Accession: T43526
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reddues: 1-469 <VBR.
A;Coss-references: EMBL:AF009512; NID:g2443510; PIDN:AAC32420.1; PID:g2443511
C;Genetics:
                                                                                                                             382
                                                                                                                                                                                                                                                                                       148
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                                                                                    325
                                                                                                                                                                        326 DDPKVSSDFLDLIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPFFVPTLKSD 382
                                                                                                                                                                                                                                                              DDTSNFDEPEKNSWVSSSPCQLSP--SGFSGEELPFVGFSYSKALGILGRSESVVSGLDS 440
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-- SNKMVNAKLPIGTPDYMA
                                                                                                             329 PEVLL-----KKGYGMECDWWSLGAIMYEMLVGYPPFYSDDPMSTCRKIVNWKNHLKFP
                                                                                                                                                                                                                   383 EEAKLSPEAKDIISRLLCNVTERLGSNGADEIKVHSWFKGIDWDRIYQMEAAFIPEVNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 HRMGYIHRDIKPDNILIDRDGHIKLSDFGLSTGFYKQDQSASYMKPRTGNTVKRGQMVDA
                                        269 PLDCSTLEEKDFSVGDNANGGSRSDSPPAPKRTQQEQLEHWQKNRRMLAYSTVGTPDYIA
                                                                                 PEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 SAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 TSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 DSPWTVSLYYAFQDSLYLYLIMEFLPGGDLMTMLINY-DTFSEDVTRFYMAECVLAIADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 HLMGYVHRDIKPENILVDRTGHIKLVDFG------SAAKM-----SAAKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T41723; T43526 TR; Riscieger, M.; Lynce, M.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1999 A; Reference number: Z22012
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26.9%; Score 700; DB 2;
Best Local Similarity 39.2%; Pred. No. 1.4e-24;
Matches 148; Conservative 63; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                     441 PAKTSSMEKKLLIKS---KBLQDSQD 463
                                                                                                                                                                                                                                                                                                                                                                                              500 LKKTNTKPKKPTIKSLFGDESEASED
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A,Map position: 1
A,Introns: 48/2; 106/3
C,Function:
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245 KMN-
                                                                                      266
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R;Huang, Y.; Wan, J.; Ko, K.; Dennis, D.T.
submitted to the EMBL Data Library, December 1992
A;Description: A cAMP-dependent protein kinase homolog in tobacco leaf.
A;Reference number: 849077
A;Molecule type: mRNA
A;Residues: 1-526 <HUX>
                                                                                                                                                                                                                     IYAMKVMKKKALLLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGD
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Search completed: March 18, 2005, 15:40:47 Job time: 45 BECS

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein March 18, 2005, 15:21:39 ; Search time 174 Seconds
 (without alignments)
 1104.712 Million cell updates/sec Run on:

US-10-724-594-2 2602 score: Perfect

1 MLKFKYGARNPLDAGAAEPI..........CSRILPSVYAKGSARGRCWL 497 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:* Database

geneseqn1980s: geneseqn1990s: geneseqn2000s: geneseqn2001s: geneseqn2001s: geneseqn2003s: geneseqn2003bs: geneseqn2003bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

	Description	Abul0126 Novel hum	Aae39504 Human kin	Ado40592 Human kin	Abp97687 Amino aci	Aae16261 Human kin	Abul0127 Variant n	Abp97681 Amino aci	Adn62809 Human NOV	Ada05644 Human NOV		Abb81927 Human kin	0 Human	Aao26959 Human CRI		Adf60994 Pain asso	Adq89100 Human uro		Adj96610 Human cit	Abg78363 RHO/RAC-i	Ada05642 Human NOV	Adn63228 Human NOV	Adn62807 Human NOV	Abg78362 Human pro		Adn62819 Human NOV
	ΙD	ABU10126	AAE39504	ADO40592	ABP97687	AAE16261	ABU10127	ABP97681	ADN62809	ADA05644	ABB81928	ABB81927	AAE24150	AA026959	AAE24079	ADF60994	ADQ89100	AAU03501	ADJ96610	ABG78363	ADA05642	ADN63228	ADN62807	ABG78362	ADA05654	ADN62819
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ALIGNMENTS

Beasley EM; Human; enzyme; gene therapy; kinase; antisense. Æ ABU10126 standard; protein; 497 11-SEP-2002; 2002US-00238709. 13-MAR-2001; 2001US-00804471. entry) (APPL-) APPLERA CORP. (first Novel human kinase. US200302340-A1. Homo sapiens. 11-AUG-2003 30-JAN-2003. ABU10126;

Di Francesco V, Webster M, Yan C,

2003-438978/41. N-PSDB; ACA61394.

New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression

Claim 1; Fig 2; 207pp; English.

The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are transgenic animals expressing all or a part of the nucleic acid, for

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monitoring the effectiveness of modulating compounds on the expression cactivity of the transporter gene in clinical trials or in treatment regimen, in gene therapy and as antisense constructs to control transporter gene expression in cells, tissue and organisms. The present sequence represents the amino acid sequence of a novel human kinase
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/note= "Protein kinase ATP-binding region signature"
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te= "Protein kinase C phosphorylation site"
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19-SEP-2002

US2002132322-A1

13-MAR-2001; 2001US-00804471.

13-MAR-2001; 2001US-00804471

(WEBS/) WEBSTER M. YANC/)

YAN C. DI FRANCESCO V.

BEASLEY E (BEAS/) Francesco V, 걾 Yan C, Webster M,

Beasley WPI; 2003-687480/65

New isolated human kinase proteins, useful as models for developing human therapeutic targets, or for treating a disorder associated with an absence of, inappropriate or unwanted expression of the protein, e.g. N-PSDB; AAD59937, AAD59938.

Claim 1; Fig 2; Opp; English.

The present invention relates to human kinase proteins and nucleic acids encoding them all of which are useful in the development of human therapeutics and diagnostic composition and methods. The invention is useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents. The invention is also useful in

us-10-724-594-2.rag

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   drug screening assays, in assays to determine the biological activity of the protein, to raise antibodies and to elicit another immune response. The antibodies are useful in pharmacogenomic analysis, for inhibiting protein function and for tissue typing. The transgenic animals are useful for studying the function of kinase protein, identifying and evaluating modilators of kinase protein activity. The invention is also used in gene therapy. The present sequence is the human kinase protein. The human kinase gene is located on chromosome 12
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                                                                                                                    Length 497;
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kinase related disorder, human, enzyme.
                                                                                                                                        0; Indels
                                                                                                                  100.0%; Score 2602; DB 7;
100.0%; Pred. No. 2.1e-254;
ive 0; Mismatches 0;
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phosphorylation site"
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Les 497; Conservative
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The present invention provides a kinase polypeptide and its encoding bolynucleotide. The polypeptide and polynucleotide of the invention are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic gents that modulate kinase activity in cells and tissues that express the kinase. The invention is also useful for biological assays related to kinases, in drug screening assays, for treating disorders characterized by an absence of inappropriate and
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                                                                                                                                         note= "Protein kinase ATP-binding region signature"
[40. .143
                                                                                                                                                                                                                                                                                                note= "Serine/Theronine protein kinase active-site
                                                                       93. .95
/note= "Protein kinase C phosphorylation site"
103. .126
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:e= "Casein kinase II phosphorylation site"
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note= "Protein kinase C phosphorylation site"
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/note= "Helix 1"
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/note= "Pro
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248. .250
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the protein. The present sequence is the human
                                                                                                                              Gaps
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                                                                                            Length 497;
                                                                                                                            Indels
                                                                                          Score 2602; DB 8;
Pred. No. 2.1e-254;
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2001US-0337130P.
2002US-0375015P.
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10-DEC-2001;
25-APR-2002;
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The present sequence represents a human citron rho/rac-interacting kinase—short kinase polypeptide. The polynuclectide and polypeptide of the invention are useful in preventing, ameliorating, or treating diseases associated with the polypeptide dysfunction. The expression vector or the reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase-short kinase in a disease, such as obesity or chronic obstructive pulmonary disease. These may also be used for treating obssity/ overweight-associated comorbidities, such as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced fertility, and depression
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Matches 496; Conservative
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Human; kinase; PXIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AlDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis; Good pasture's syndrome; Graves' disease; pancreatitis; psorianis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; haparitis; hypothyroidism; cerebral palsy; cararact; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy.
                                                                                                                                                                                                                                        Location/Qualifiers
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AAE16261 standard, protein, 497
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30-JUN-2000; 2000US-0215651P.
07-JUL-2000; 2000US-0216605P.
13-JUL-2000; 2000US-0218372P.
25-AUG-2000; 2000US-0228056P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2001; 2001WO-US019444
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                                                              Human kinase PKIN-7 protein
                                           (first entry)
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                                                                                                                                                                                                                  Homo sapiens
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                                           26-MAR-2002
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                     AAE16261;
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97. .360
/note= "Bukaryotic protein kinase 98. .241
/label= Protein_kinase_domain
86. .124
/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

WPI; 2002-090207/12 N-PSDB; AAD26454. New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as

RESULT 6 ABU10127

The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition associated with decreased expression of reating a disease or condition associated with decreased expression of PKIN and a composition associated with decreased expression of PKIN and a composition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The composition of the composition ö 240 120 120 180 300 300 180 240 360 360 420 420 480 480 9 9 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE ECSQPALMKIKHVSNPVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 61 ECSOPALMKIKHVSNFVRKYSDTIAELOELOPSAKDPEVRSLVGCGHFAEVQVVREKATG 181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 241 GSAAKMISNKWWAKLPIGTPDYMAPEVLTWMNGDGKGTYRLDCDWWSVGVIAYEMIYGR 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 241 GSAAKMISIKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 301 SPFAEGTSARTFUNIMNFORFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 301 SPFAEGTSARTFUNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 361 SKIDWANIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSELPFVGFS 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR ö 99.5%; Score 2589; DB 5; Length 497; 99.6%; Pred. No. 4.5e-253; ive 1; Mismatches 1; Indels C cancer, comprise human kinase polypeptides. English 497 497 Claim 1; Page 146-147; 197pp; 481 ILPSVYAKGSARGRCWL 481 ILPSVYAKGSARGRCWL Best Local Similarity 99.6 Matches 495; Conservative Sequence 497 AA; PKIN-7 protein 19 121 181 Query Match a 8 셤 a 셤 셤 셤 ò 셤 Š ò ⋩ ઠે 8

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The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic proteins, and serve as targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic gapnts that modulate kinase activity in cells and tissues that express the kinase. The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for monitoring the effectiveness of modulating compounds on the expression or equivity of the transporter gene expression in cells, tissue and organisms. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is not shown in the specification but indexer using the information given in figure 3
                                                                                                                                                                                                                                                         /note= "Wild-type Trp substituted by Cys as a result of single nucleotide polymorphism"
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                                                                                                                                             gene therapy; kinase; antisense.
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ABU10127 standard; protein; 497
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                                                                                                            Variant novel human kinase.
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                                                                                                                                                Human; enzyme;
                                                                                                                                                                                   Homo sapiens
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                                                                         1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
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 Length 497;
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99.5%; Score 2589; DB 6;
99.8%; Pred. No. 4.5e-253;
iive 0; Mismatches 1;
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Matches 496; Conserv
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ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHPAEVQVVREKATG 120

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121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

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361 SKIDCNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGEELPFVGFS
                                                                                                                                                                                                                                                                                              421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR
                                             DLLSLLNRYEDQLDENLIQFYLAEL1LAVHSVHLMGYVHRD1KPEN1LVDRTGH1KLVDF
                                                             DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                                                                                                    GSAAKMISIKMINAKLPIGTPDYMAPEVLTVMIGDGKGTYGLDCDWWSVGVIAYEMIYGR
                                                                                                                       241 GSAAKANSNKAVNAKLPIGTPDYMAPEVLTVANGDGKGTYGLDCDWHSVGVIAYEMIYGR
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2002US-0375015P.
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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 100-101; 586pp; English

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of sorreming for a modulator of activity or of latency or predisposition to a pathology associated with the above polypeptide in a commanal; and (14) a method for producing the above polypeptide in a commanal; and (14) a method for producing the above polypeptide in a commanal; and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a colypeptide is useful in manufacturing a medicament for treating and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating and antilipaemic activities, and can be used in gene therapy. The colypeptide is useful in manufacturing a pathology associated with a hardson or prevent metabolic acid molecule may be used to diagnose, treat or prevent metabolic collected in the parafer pharmacogenomics. The present sequence represents a human NOVX from the present invention. disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine an

Sequence 623 AA;

240 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 184 SPFAEGTSARTFANIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 364 9 64 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFB GSAAKMISIKOVIVAKLPIGTPDYMAPEVLTVMKGDGKGTYGLDCDWSVGVIAYEMIYGR 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE DLLSLLNRYEDQLDENLI QFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF Gaps ; 0 Length 623; 0; Indels Score 2440; DB 6; Pred. No. 8.6e-238; 2; Mismatches 0; 93.8%; Matches 466; Conservative Best Local Similarity 245 ß Query Match 61 9 121 125 181 185 241 301 d 셤 ઠે 셤 õ 셤 õ 셤 Š 8

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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly citron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polymucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The 424 120 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHPAEVQVVREKATG 120 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180 361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420 9 9 in gene Human, kinase, enzyme, serine-threonine kinase, nootropic, cytostatic, Citron rho-interacting kinase, gene therapy, mental disorder, cancer. 365 SKIDWANIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG Gaps Novel polynucleotide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, in therapy of disorders and diseases e.g. cancer and pharmacogenomic applications. ; 472 425 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV sequence represents a novel human kinase of the invention Indels ö Score 2440; DB 5; Pred. No. 5.7e-237; 2; Mismatches ABB81928 standard; protein; 1958 AA Claim 4; Page 46-50; 50pp; English. Miranda M, Friddle CJ 20-DEC-2001; 2001WO-US050497. (LEXI-) LEXICON GENETICS INC. 27-DEC-2000; 2000US-0258335P. 93.8%; (first entry) Matches 466; Conservative WPI; 2002-599796/64. Local Similarity Sequence 1958 AA; N-PSDB; ABQ78871 WO200259325-A2 Homo sapiens. Human kinase 10-OCT-2002 01-AUG-2002. ABB81928; Query Match ۲a x, RESULT 10 **ABB8192** a 셤 셤 ò ઠે

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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly Citron rho-interacting Kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence represents a novel human kinase of the invention
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Citron rho-interacting kinase; gene therapy; mental disorder;
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                                                       Indels
Score 2440; DB 5;
Pred. No. 6.1e-237;
2; Mismatches 0;
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/note= "Protein kinase domain"
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Query Match
Best Local Similarity 99.6%;
Matches 466; Conservative
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong Ji W, Miller CE, Raetelli L, Stone DJ, Pena CEA,
                                                       2001US-0326483P.
2001US-0327443P.
2001US-0327444P.
2001US-0328029P.
2001US-0328044P.
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SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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BERGHS C.
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EISEN A.
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RIEGER D K.
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RASTELLI L.
STONE D J.
SHONA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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ZERHUSEN B D.
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PEYMAN J 1
KEKUDA R.
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reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinage-short kinage in a disease, such as obesity or chronic obstructive pulmonary disease. These may also be used for treating obesity/ overweight-associated comorbidities, auch as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced fertility, and depression
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the polypeptide dysfunction. The expression vector or the
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associated with
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Li L, Guo X;
Malyankar UM;
M, Catterton E;
Shenoy SG;

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The invention relates to isolated NoVX polypeptides and polymucleotides.

NoVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abberrant expression and activity of NoVX polypeptides. For example, NoVX polypeptides and activity of NoVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NoVX polypucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NoVX polypeptides and sassays to identify modulators the production of antibodies and in assays to identify of NoVX. The anti-NoVX polypeptide and indices and antagonists and antagonists and antagonists and antagonists and antagonists and activity of NoVX. Coused to modulate NoVX polypeptide expression and activity of NoVX polypeptides. The anti-NoVX polypeptide antibodies may also be used as diagnose and treat: metabolic disorders, diabetes, obesity, infectious diagnose and treat: metabolic disorders, diabetes, obesity, infectious dispundences associated with obesity, the metabolic syndrome X and chematopoietic disorders, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic conference of a human NoVX protein.
    Berghs C, Dipippo VA;
                                                                                                                                       Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
  rg ME, Leach MD, Agee ML
Rieger DK, Spaderna SK;
                                                                                                                                                                                                             Claim 1; SEQ ID NO 4; 395pp; English
  RA, Rothenberg ME,
Gangolli EA, Rieg
                                                                   WPI; 2004-213931/20.
N-PSDB; ADN62808.
Shimkets RA,
                        Eisen A,
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Sequence 620 AA;

240 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180 GSAAKMISIKMYNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 304 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFGLCCHPFF 364 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420 64 125 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG S MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE GSAAKMINSINKMYNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR SPFAEGTSARTFINITMNFORFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 0; Gaps Query Match
93.8%; Score 2440; DB 8; Length 620;
Best Local Similarity 99.6%; Pred. No. 8.5e-238;
Matches 466; Conservative 2; Mismatches 0; Indels 61 121 181 185 245 301 305 361 365 241

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WPI; 2003-381626/36. N-PSDB; ADA05643

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Dipippo VA;
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                                                                                                                                                                                             immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                    human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
            425 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 472
421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV
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                                                                                   ADA05644 standard; protein; 623
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15-007-2001;
17-007-2001;
24-007-2001;
24-007-2001;
24-007-2001;
29-007-2001;
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19-APR-2002; 2
19-APR-2002; 2
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Qy 181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHII		දු පු	361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFEGEELPFVGFS 420
Qy 241 GSAAKMISNKAYNAKLPIGTPDYMAPEVLTVANGDGKGTYGLDCDWWSVGVIAYER	remiygr 300 remiygr 300	<i>ò</i> 8	421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVPISAAGLLPCSR 480
OY 301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIGSLLCGGKERLKFEGLCC 	CCHPFF 360	<i>≿</i> 43	481 ILPSVYAKGSARGRCWL 497 481 ILPSVYAKGSARGRCWL 497
QY 361 SKIDWNNIRNSPPFFVPTLKSDDDTSNFDEDEKNSWYSSSPCQLSBSGFSGEELP!	DEVGFS 420	RESULT US-10-7	3 24-594-2 100-7-1 interior TE/10704E04
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 	JLLPCSR 480	; Seque ; Publ: ; GENE	; Sequence 7, Application 05/10/4354; Sequence 7, Application No. US20040091993A1; GENERAL INFORMATION: APPLICANT: WEBSTER, Marion et al.
Oy 481 ILPSVYAKGSARGKUL 497		rie ;	E OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC E OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES E OF INVENTION: THEREOF
Db 481 ILPSVYAKGSARGRCWL 497			REFERENCE: CLOO1164DIV II RENT APPLICATION NUMBER: US/10/724,594
RESULT 2 US-10-238-709-2 : Seruence 2. Application US/10238709		SEO	NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
; Publication No. US20030022340A1 ; GENERAL INFORMATION: ; APPLICANT: WEBSTER, Marion et al			LENGTH: 497 TYPE: PRT ORGANISM: Homo sapiens
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC	SEST ON SE	01-sn	
TILLE OF INVENTION: ACLE POLICOLE TILLE OF INVENTION: THEREOF FILE REPERENCE: CLOOLI64DIV CURRENT APPLICATION NUMBER: US/10/	e e e e e e e e e e e e e e e e e e e	Query Ma Best Loc Matches	/ Match 100.0%; Score 2602; DB 15; Length 497; Local Similarity 100.0%; Pred. No. 4.9e-190; Anniarity 0; Gaps 0; Indels 0; Gaps 0;
; CURRENT FILING DATE: 2002-09-11 ; NUMBER OF SEQ ID NOS: 4 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2		රු සි	1 MLKEKYGABNPLDAGAAEPIANRASRLNLFFOGKPPFMTQQQMSPLSREGILDALFVLFE 60
; LENGTH: 497 ; TYPE: PRT ; ORGANISM: Human US-10-238-709-2		& q	61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSIVGCGHFAEVQVVREKATG 120
Query Match 100.0%; Score 2602; DB 14; Length 497; Best Local Similarity 100.0%; Pred. No. 4.9e-190; Matches 497; Conservative 0; Mismatches 0; Indels 0;	Gaps 0;	& g	121 DIYAMKVMKKKALLAQEQVSFFEBENILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
1 MLKFKYGARNPLDAGAAEPIANRASRLMLFFQGKPFFMTQQQMSPLSREGILDAI 	ALFVLFE 60	& g	181 DLLSLINRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
Qy 61 ECSQPALMKIKHVSNPVRKYSDTIAELQELQPSAKDFEVRSLVGCGHPAEVQVVREKATG	VREKATG 120 VREKATG 120	. ර් යි	241 GSAARONSNROWVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300 241 GSAARONSNROWVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
Oy 121 DIYAMKVMKKKALLAQEQVSFFEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG	MEYQPGG 180	У да	301 SPFABGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
Qy 181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHT:	HIKLVDF 240	රු සි	361 SKIDWNNIRNSPPFVPTLKSDDDTSNFDEPERNSWSSSPCQLSPSGFSGEELPFVGFS 420
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Qy 301 SPFAEGTSARTFNNIMNPQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLC 	LCCHPFF 360 LCCHPFF 360	Oy Op	481 ILPSVYAKGSARGRCWL 497 481 ILPSVYAKGSARGRCWL 497
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March 18, 2005, 15:40:07; Search time 146 Seconds (without alignments) 1125.198 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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8	2602	100.0	497	14	US-10-238-709-2	Sequence 2. Appli
٣	2602	100.0	497	15	US-10-724-594-2	Sequence 2, Appli
4	2589	99.5	497	15	US-10-311-034-7	Sequence 7, Appli
G	2440	93.8	623	15	US-10-262-511-4	Sequence 4, Appli
9	2440	93.8	1958	13	US-10-028-946-4	Sequence 4, Appli
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α0	2440	93.8	2054	15	US-10-415-011-21	Sequence 21, Appl
o,	2430	93.4	2053	13	US-10-017-216-2	Sequence 2, Appli
10	2430	93.4	2053	14	US-10-325-430-12	Sequence 12, Appl
11	2430	93.4	2053	16	US-10-757-262-52	Sequence 52, Appl
12	2418.5	92.9	2055	16	US-10-618-941-67	Sequence 67, Appl
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US-10-262-511-2 Sequence 2, Appli US-09-964-956-9 Sequence 9, Appli	511-14 Sequence	71A-4 Sequence 4	709-4 Sequence 7594-4	Sequence	897-2 Sequence	048-2 Sequence	048-4 Sequence	048-5 Sequence	048-6 Seguence (496-2 Sequence	011-2 Sequence	314-20 Sequence 2	941-68 Sequence (493-6347 Sequence 63	-697-1540 Sequence 154	161A-219 Sequence 219,	161A-220 Sequence 220,	US-10-399-225-10 Sequence 10, Appl	-581-206 Sequence 200)-753-267-72 Sequence 72,	-771-161A-228 Sequence 228,)-288-798-2 Sequence 2,	892-2 . Sequence 2,	Seguence 19,	496-4 Seguence 4,	130-102 Sequence 103	0-130-100 Sequence 100	-764-868-671 Sequence 671,	9-764-875-1205 Sequence 120	OHNDRING 1
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ALIGNMENTS

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Sequence 2, Application US/09804471A
Patent No. US20020132322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THERED MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERED WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERED WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERED WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERED WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
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CURRENT PILING DATE: 2010-03-13
NUMBER OF SEQ ID NOS: 4
IENGTH: 497
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ORGANISM: Human
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catherosclerosis, multiple sclerosis, psoriasis), disorders affecting growth and development (e.g., arreniosclerosis, cirrhosis, hepatitis), cardiovascular disorder (e.g., hypertension, myocardial infarction, Goodpasture's syndrome), and a lippid disorder (e.g., fatty liver, Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia, hyperstipidaemia, obesity), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a disquestic test for a condition or a disease associated with the expression of PKIN in a condition or a disease associated with the expression of FKIN in a antagonist of PKIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN. PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, and in somatic or germline gene therapy. The present sequence is human

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Sequence 2054 AA; PKIN protein

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Lal PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders.
                                                                                                                                                                                                                                       "note= "Domain found in NIK1-like kinase"
1390. .1438
'note= "Phorbol esters/diacylglycerol binding site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C; Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB; R, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, 18A, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;
                                                                                                                // Anotes "Leucine zipper pattern"
// notes "Leucine zipper pattern"
// 1015. .1067
// 1018. .1078
// notes "Leucine zipper pattern"
// notes "Leucine zipper pattern"
// 1159. .1180
// notes "Leucine zipper pattern"
// notes "Domain found in NIK1-like kinase"
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1851. .1880
/note= "Domain found in NIX1-like kinase"
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1819. .1831
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                                                  'note= "Protein kinase domain"
                     "Protein kinase
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'note= "PH domain"
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; 2000US-0244068P.
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; 2000US-0247672P.
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                                                                                                                                                                                                                               DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG
                                                                                                                                                                                                                                                                                                                                                                                                        241 GSAAKONSNKWVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR
                                                                                                                 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE
                                                                                                                                                     ECSOPALMKI KHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
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                                       0; Gaps
Score 2440; DB 5; Length 2054;
Pred. No. 6.1e-237;
2; Mismatches 0; Indels 0
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 Query Match 93.8%;
Best Local Similarity 99.6%;
Matches 466; Conservative
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The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing, treating and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,

360 360 420

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361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
                                            241 GSAAKANSNKAVNAKLPIGTPDYMAPEVLTVANGDGKGTYGLDCDWWSVGVIAYEMIYGR
                                                                                                                           SPFAEGTSARTFINIMINFORFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF
                                                                                                                                                                                            361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein; tumourigenesis; tumour growth; tumour metastrasis; viral infection; skeletal muscle disorder; muscular dystrophy; myotonic dystrophy; immune disorder; neoplastic disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Serine/Threonine protein kinase active site
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                                                                                                                                                                                                                                                                                                      YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468
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1568. .1865
/note= "CNH domain"
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195. .2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD39191
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polymucleotide encoding a human citron rho/rac-interacting kinase polypeptide. The isolated control to the polymucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK) polypeptide and polymucleotide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hypertipidaemia, stroke, gout, osteoarthritis, some types of cancer including endomerrial, breast, prostate and colon cancer), anorexia, cachexia, bullmia, central nervous system disorders (e.g. mood disease), chronic obstructive pulmonary disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary central nervous system disorder, or chronic obstructive pulmonary contral nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a cancer in producing and detecting the polymucleotide and polypeptide and consecutive pulmonary colypeptide. This sequence represents the human CRIK protein of the human CRIK protein of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human citron rho/rac-interacting kinase (CRIK) polypeptide polymorlectide, useful in preventing, ameliorating or treating associated with human CRIK dysfunction, e.g. obesity, diabetes Alzheimer's disease.
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11-DEC-2001; 2001US-0338651P.
25-APR-2002; 2002US-0375014P.
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                                                                                   WO2003004523-A1
diabetes; pain.
                                          Homo sapiens
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(MDPK) polypeptides designated as 13245 and nucleic acid molecules encoding such polypeptides. 13245 molecules are used to develop diagnostic and therapeutic agents for prognosticating, diagnosing, preventing, inhibiting, alleviating or curing MDPK-related disorders. Polypeptides of the invention are used to develop diagnostic and therapeutic agents for 13245-mediated or related disorders such as tumourigenesis tumour growth, tumour metascasis, viral infection of a cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies), immune disorders and neoplastic disorders. The invention is also used in gene therapy. The present sequence is human MDPK protein
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                                                                                                                                                                                                                                                                                                           BCSQPALMKIKHVSNFVRKYSDTIABLQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
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                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                      Query Match
93.4%; Score 2430; DB 5;
Best Local Similarity 99.1%; Pred. No. 6.3e-236;
Matches 464; Conservative 3; Mismatches 1;
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                                                                                                                                                                                        Sequence 2053 AA;
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The present invention relates to a method for identifying a compound capable of modulating pain or painful disorders. The method comprises assaying the ability of the compound to modulate specific nucleic acid expression or polypeptide activity e.g. potassium channel, or kinase expression/activity. The method and compounds are useful for treating pain or painful disorders e.g. inflammatory pain, chronic pain, neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache pain and tissue pain. The present sequence represents a human protein associated with pain.
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Pred. No. 6.3e-236;
3; Mismatches 1;
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19-DEC-2001; 2001US-0341953P
                                     (MILL-) MILLENNIUM PHARM INC
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Best Local Similarity 99.1
Matches 464; Conservative
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Job time : 179 secs

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Sequence 1, Appli
Sequence 29273, A
Sequence 21232, A
Sequence 11, Appl
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Sequence 17152, A
Sequence 1315, Ap
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Sequence 57, Appli
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO1_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USO1_NEW_COMB.seq:*

9: /cgn2_6/ptodata/2/pna/USO1_NEW_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-450-763-15557
US-10-450-763-29273
US-10-450-763-13871
PCT-US03-11189-11
PCT-US03-11189-13
PCT-US03-11189-13
US-11-060-756-1334
US-11-060-756-1335
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US-11-060-756-5606
US-11-060-756-5606
US-10-073-11189-6
PCT-US03-11189-6
PCT-US03-11189-8
US-10-932-182A-150
US-10-932-182A-150
US-10-932-182A-1910
PCT-US03-11189-8
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Sequence Sequence

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Gaps

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Length 1048; Indels 74

134 235 194 295 355 314 415 374 475

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614 715 674 775 734 835 794 895 854 955

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236 GAAGGGATATTAGATGCCCTCTTTGTTTTTTTTTTTTGAGAATGCAGTCAGCCTGCTCTGATG
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                                                                   CGGAATCCTTTGGATGCTGGTGCTGAACCCATTGCCAACCGGGCCTCCAGGCTGAAT
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Score 925; DB 7; I
Pred. No. 3.7e-235;
0; Mismatches 5;
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18.10-450-763-29273

1 Sequence 29273, Application US/10450763

1 GENERAL INFORMATION:
Query Match
Best Local Similarity 99.5%;
Matches 928; Conservative
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                                                              CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG
                                                                                  CTATGAAAGTGATGAAGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG
                                                                                                                                                 CACTITIGATAGATAAGATGAAGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG
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GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG
                                                                                                                              AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCT
                                                                                                                                                                                                                                                                 CACTITIGAATAGATAGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG
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LOCATION: (412)...(909)
OTHER INFORMATION: 77% homologous to Mus musculus Pro-Pol-dUTPase
OTHER INFORMATION: polyprotein, accession number Y12713, Smith-Waterman
US-10-450-763-15557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAG 957
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLIS
FILE REPERENCE: 790CT93/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT PILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
SOFTWARE: CUSTOM
SOFTWARE: CUSTOM
SOFTWARE: CUSTOM
SEQ ID NOS: 60736
SETURING: 100 NOS: 60736
SEMINANTE: 1048
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US-10-450-763-15557
; Sequence 15557, Application US/10450763
; GENERAL INFORMATION:
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NAME/KEY: SIMILAR
LOCATION: (3137)...(5767)
OTHER INFORMATION: 79% homologous to Homo sapiens Human myotonic dystrophy gene
OTHER INFORMATION: protein, accession number R41001, Smith-Waterman Score=3811.
                                                                                                                                                                                                                                                                                                                                                      1015
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                                                                                                                                                                                                                                                                                                                                                                                                         1018 GCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC------CATCCTTTCT 1068
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                                                                                                                                                                                                961 TTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCTGATTCAAAGCTTGTTGT
                                                                                                                                                                                                                                                   184 CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAG
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PLILIATION NUMBER: CT/US01/08631
PRIOR PLILIATION NUMBER: 09/540,217
PRIOR PLILING DATE: 2000-03-30
PRIOR PLILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 21232
LENGTH: 6303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1129 AGTCCGACGATGACACCTCCAATTTTGA 1156
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US-10-450-763-21232
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OTHER INFORMATION: 31% homologous to Homo sapiens Human myotonic dystrophy
OTHER INFORMATION: protein, accession number R41001, Smith-Waterman Score=77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
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## APPLICANT: Hyseq, Inc

### TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

### FILE REPERENCE: 790C1P3/US

### CURRENT APPLICATION NUMBER: US/10/450,763

### CURRENT PILING DATE: 2003-06-11

### PRIOR APPLICATION NUMBER: PCT/USO1/08631

### PRIOR PLILING DATE: 2001-03-30

### PRIOR PILING DATE: 2000-03-31

### PRIOR PLILING DATE: 2000-03-31

### PRIOR PLILING DATE: 2000-03-31

### PRIOR PLILING DATE: 2000-08-23

### NUMBER OF SEQ ID NOS: 60736

### SOOFTWARE: CUSTON

### SEQ ID NO 29273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.2%; Score 225.6; DB 7; Length 1 Best Local Similarity 54.0%; Pred. No. 5.9e-50; Matches 534; Conservative 0; Mismatches 439; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 13811, Application US/10450763
GENERAL INFORMATION:
APPLICANT: Hyeeq, Inc.
TILLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL;
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
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LENGTH: 5754 TYPE: DNA ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)...(411)
; OTHER INFORMATION: 95% homologous to Escherichia coli RF-3/Tos, accession number:
; OTHER INFORMATION: D17724, Smith-Waterman Score=665.
US-10-450-763-13871
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                                                                                                                                                                                                          Score 213.2; DB 7;
Pred. No. 1.6e-46;
0; Mismatches 553;
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Best Local Similarity 50.9%;
Matches 590; Conservative
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Pred. No. 5.5e-42;
0; Mismatches 570; Indels
                                                                       TYPE: DNA
ORGANIEM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Refeeq / NM 053620
DATABASE ENTRY DATE: 2003-10-05
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.5%;
Matches 573; Conservative
       script
  SOFTWARE: Perl
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                           SEQ ID NO 13
LENGTH: 5333
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GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REPERENCE: 17633/2048
CURRENT APPLICATION NUMBER: PCT/US04/42360
CURRENT FILING DATE: 2004-12-17
PRIOR FILING DATE: 19-Dec-2003
NUMBER OF SEQ ID NOS: 2587
CGGCTGGGGCAGAATGGAATAGAGGATTTCAAAAAGCATGCGTTTTTTGAAGGTCTAAAT 1038
                                                                                              TGGGAAAATATACGAAACCTAGAAGCACCTTATATTCCTGATGTGAGCAGTCCCTCTGAC 1098
                                                                                                                                                ACCTCCAATTTTGATGAACCAGAGAAGTTCGTGGGTTTCATCCTCTCTCGTGCCAGCTG 1202
                                                                                                                                                                                            ACATCCAACTTCGACGTGGATGACGACGTGCTGAGAAACACGGAAATATTACCTCCTGGT 1158
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
FILE REFERENCE: D0193 PCT
CURRENT APPLICATION NUMBER: PCT/US03/11189
CURRENT PLILING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATCHIN VERSION 3.2
SEQ ID NO 11
LENGTH: 204
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Pred. No. 4.5e-44;
0; Mismatches 1;
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Best Local Similarity 99.5%;
Matches 203; Conservative (
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ORGANISM: Homo sapiens
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PCT-US03-11189-11
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GENERAL INFORMATION:
APPLICANT Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL POLYPEPTIDE, BMSNKC_0020/0021
FILLE REPERENCE: D0193 PCT
FILLE REPERENCE: D0193 PCT
CURRENT APPLICATION NUMBER: PCT/US03/11189
CURRENT FILLING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-12
PRIOR PLILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIB3/U0
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
FRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
FRIOR FILING DATE: 2000-03-31
FRIOR APPLICATION NUMBER: 09/540,217
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11.9%; Score 176; DB 1; 1
Best Local Similarity 100.0%; Pred. No. 4.2e-37;
Matches 176; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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NAME/KEY: SIMILAR
LOCATION: (1341)..(3980)
OTHER INFORMATION: 100% homologous to Homo sapiens myotonic dystrophy protein
OTHER INFORMATION: kinase like protein, accession number Y12337, Smith-Waterman Score-
OTHER INFORMATION: 969.
FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
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Pred. No. 1.3e-36;
0; Mismatches 229;
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; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-17152
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Best Local Similarity 58.4%;
Matches 326; Conservative
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 17152
LENGTH: 4055
                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: Wyeth
APPLICANT: Woth
APPLICANT: Woth
APPLICANT: Mounts, William Martin
AITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 5607
LENGTH: 489
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
FILE REFERENCE: DOLYDEPTIDE, BMSNKC_1020/0021
CURRENT APPLICATION NUMBER: PCT/US03/11189
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: U.S. 60/372,745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 171.8; DB 8;
Pred. No. 7.2e-36;
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98.9%; Pred. No. ....
0; Mismatches
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GENERAL INFORMATION:
                              NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 5606
LENGTH: 489
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Best Local Similarity 98.9
Matches 173; Conservative
                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-11-060-756-5606
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ORGANISM: Homo sapiens
US-11-060-756-5607
          CURRENT FILING DATE:
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REPERENCE: AMIO1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT APPLICATION NUMBER: US/11/060,756
NUMBER OF SEQ ID NOS: 303284
SEQ ID NOS: 303284
SEQ ID NO 1335
LENGTH.
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031856-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
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                                                                                                                                                                                                                                               Score 171.8; DB 8; Length 489;
Pred. No. 7.2e-36;
0; Mismatches 2; Indels 0
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CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SSOFTWARE: PatentIn vergion 3.2
LENGTH: 489
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Best Local Similarity 98.9%;
Matches 173; Conservative
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Best Local Similarity 98.9
Matches 173; Conservative
                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-060-756-1334
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US-11-060-756-1335
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Sequence 6, Application PC/TUS0311189
Sequence 6, Application PC/TUS0311189
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEGOTIDES ENCODING THE HUMAN CITRON KINASE
TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
FILE REFERENCE: D0193 PCT
CURRENT APPLICATION NUMBER: PCT/US03/11189
CURRENT FILING DATE: 2003-04-11
FRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 142
                                                                                                                                                                                                                                                                                                                507 GTCATGGAATATCAGCCTGGAGGGACTTGCTGTCACTTTTGAATAGATATGAGGACCAG 566
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PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LENGTH: 143
                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
PCT-US03-11189-9
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ORGANISM: Homo sapiens
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COMB. Beq: *
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Н	'n	e 9	'n	9	'n	e,	7	43,	767	Sequence 3, Appli	넊	e 1	, 0	S.	HÌ.	ĭ	5	ce 4	٦,	, ,	1, Appli	; 0	1, Appl	ω	m,	ω,		13,	10474, A	ce 104	416,	419,	41	e 1,	155	l, Appl	1082,	e 1082,	10200,	30150,	3015	equence 15814,	Sequence 15814, A	Seguence 45643, A
SUMMARIES ID		US-10-724-594-1	US-10-311-034-	US-60-215-651-	PCT-US02-31	US-10-262-511-	US-10-262-511A	US-10-791	US-10-791-666-	US-10-415-011	US-10-170-235-	US-10-017-216-	PCT-US02-41011-1	US-10-325-430-	-41011-1	PCT-US04-00750-	US-10-017-216-1	US-10-325-430-1	US-10-757-262-51	5 US-60-457-901	PCT-US03		PCT-US02-31373-1	US-09-964-956	US-10-262-511-1	US-10-262-511A-1	373-1		-262	US-10-262-511A-13	US-10-144-771-10474	6 US-60-360-207-1	PCT-US02-01222-41	US-10-120-988-4	US-10-470-868-41	US-10-412-897-1	PCT-US01-08631-15557	PCT-US02-23268-1	US-10-932-349-	0 US-60-500-337	US-09-699-998-1	US-09-785-276A	US-10-357-930-301	US-09-785-276A-158	US-10-357-930-158	US-09-785-276A-45643
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ALIGNMENTS

Sequence 1, A	ULT 1 10-724-594-1 sequence 1, Application US/10724594 sequence 1, Application US/10724594 sequence 1, Application US/10724594 september 1 in FormArion: TIPLE OF INVENTION: ORGANISM: ORGANISM: TOTAL OF THE OF INVENTION: ORGANISM: TOTAL OF THE OF INVENTION: TIPLE OF THE	a similarity 100.0%; Score 1481; DB 62; Length 1515; Similarity 100.0%; Pred. No. 0; 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 TCAAATARGGAGGGGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGG 60	1 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120 	CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAGAAAGGAGTC 180	1 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240 	TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300 	GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360 	CTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420 	1 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAGTATGCCT 480	TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGACTTGCTGT 540 	CACTITICAAIAGAIAIGAGGACCAGIIAGAIGAAAACCIGAIACAGIITITACCIAGCIG 600 	AGCTGATTTTGGCTGTTCACAGGGTTCATCGGGATACGTGCATCGAGACATCAAGC 660 	CTGAGAACATTCTCGTTGACCGCACAGACACATCAAGCTGGATGTTTGGATCTGCCG 720	1 CGAAAATGAATTCAAACAAGATGGTGAATGCCCAAACTCCCGATTGGGACCCCCAGATTACA 780
		Query Matc Best Local Matches 14	н			18				4 43					

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FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
FOLD APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3951059CB1
US-10-311-034-33
                                                                                                                                                                                                   APPLICANT: DING, Li
APPLICANT: GRETHER, Megan
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATTA, Sajeev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
                                                                   HAFALIA, April
ARVIZU, Chandra S.
GURURAJAN, Rajagopal
IO, Terence P.
                                                                                                                                                                                        POLICKY, Jennifer L
                                                                                                                                     KHAH, Farrah A.
RECIPON, Shirley A.
AZIMZAI, Yalda
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Best Local Similarity 99.8%;
Matches 1478; Conservative
                                   HE, Ann
THORNTON, Michael
                   BAUGHN, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
   TANG, Y. TOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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SEQ ID NO 33
LENGTH: 2066
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737 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 796
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RESULT 2
US-1031-034-33
Sequence 33, Application US/10311034
Sequence 33, Application US/10311034
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti
APPLICANT: BANDWAM, Olga
APPLICANT: BANDWAM, Olga
APPLICANT: BANDWAM, Nark L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: GREENWALD, Sara R.
APPLICANT: GREENWALD, Sara R.
APPLICANT: GREENWALD, Sara R.
APPLICANT: REARNEY, Liam
APPLICANT: KEARNEY, Liam
APPLICANT: KEARNEY, Liam
APPLICANT: REARNEY, Liam
APPLICANT: BUGUEN, Danniel B.
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181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA

6. B 6 B 6 B 6 B 6

264 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGAACTTCGAAGTCAGAAGTCTTGTAG 323

GITGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360

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324 GTTGTGCTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGGACATCTATG

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384 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG

241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300

480

421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCT

444 AAGAGCGGAACATATTATCTCGAAGCACACAAGCCCGTGGATCCCCCAATTACAGTATGCCT

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RESULT 3
US-60-215-651-9
; Sequence 9, Application US/60215651
; GENERAL INFORMATION:

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Query Match . 93.7%; Score 1388.2; Best Local Similarity 99.8%; Pred. No. 0; Matches 1390; Conservative 0; Mismatches
                                                              Ju, Jingfang
Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Curagen Corporation
Smithson, Glennda
Millet, Isabelle
Peyman, John A.
                                                                                                                                                                                             Zerhusen, Bryan D. Anderson, David W. Zhong, Mei Zhong, Mei Zhong, Mei Zhong, Miller, Charles E. Rastelli, Luca Stone, David J. Pena, Carol E. A. Shenoy, Suresh G. Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                             Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
                                                                                                                                                                                      Gorman, Linda
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PCT-US02-31373-3
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ORGANISM: 268667493
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                                                                 AGCTGATTTTGGCTGCTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
                                                                                                                    CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
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                                                 CACTITIGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG
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PRIOR APPLICATION NUMBER: 10/262,511
PRIOR PELING DATE: 2003-00-1
PRIOR PELING DATE: 2002-10-01
PRIOR PELICATION NUMBER: 60/326,483
PRIOR PELICATION NUMBER: 60/326,483
PRIOR PELING DATE: 2001-10-02
PRIOR PELING DATE: 2001-01-02
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-10-09
PRIOR PELING DATE: 2002-10-09
PRIOR PELING DATE: 2002-05-17
PRIOR PELICATION NUMBER: 60/328,029
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-04-17
PRIOR PELING DATE: 2002-04-19
PRIOR PELICATION NUMBER: 60/373,826
PRIOR PELICATION N APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-4622-061
CURRENT APPLICATION NUMBER: PCT/US02/31373
CURRENT FILING DATE: 2003-09-28 DB 1; Length 1870; ö Indels ë.

1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATGCCAACCGGG

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0y 1141 ACACCTCCAATTTGATGAACCAGAGAAGTTCGTGGGTTTCATCCTCCGTGCCAGC 1200 1164 ACACCTCCAATTTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCCGTGCCAGC 1223 1164 ACACCTCCAATTTTGATGAACCAGAAGAATTCGTGGGTTTTCGTACAGCCAGC	-3 Application US/102 ORMATION: Smithson, Glennda Millet, Isabelle Peyman, John A. Kekuda, Ramesh Ju, Jingfang Li, Li Guo, Xiaojia (Sas Patturajan, Meera Spytek, Kimberly Edinger, Kalmerly Edinger, Karen		APPLICANT: Age, MICHELS H. APPLICANT: BEIGHS, CONSTANCE TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REPERENCE: 21402-462C CURRENT APPLICATION NUMBER: US/10/262,511 CURRENT FILING DATE: 2003-05-28 FRIOR APPLICATION NUMBER: 60/373,815 FRIOR APPLICATION NUMBER: 60/373,815 FRIOR APPLICATION NUMBER: 60/327,917 FRIOR APPLICATION NUMBER: 60/327,917 FRIOR APPLICATION NUMBER: 60/327,917 FRIOR APPLICATION NUMBER: 60/321,642 FRIOR PILING DATE: 2001-10-09 FRIOR PILING DATE: 2002-05-17 FRIOR APPLICATION NUMBER: 60/321,038 FRIOR PILING DATE: 2002-05-16 FRIOR PILING DATE: 2002-05-16 FRIOR PILING DATE: 2002-05-16 FRIOR PILING DATE: 2002-05-16 FRIOR PILING DATE: 2001-10-09
24 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGAACCCATTGCCAGCCGGG 83 61 CCTCCAGGCTGAATCTTCTCCAGGGGAAACCACCCTTATGACTCAACAGCAGATGT 120 84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 143 121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCTCTTTTTTGTCCTCTTTGAAGAATGCAGTC 180 144 CTCCTCTTTCCCGAGAGGGATATTAGATGCCTCTTTTGTCCTGTTCTTTTGAAGAATGCAGTC 203 181 AGCCTGCTCTTAGAAGAATTAAATGACCTCTTTTTTTTCCTTTTTTAAGAATGCAGTC 203 182 AGCCTGCTCTGATGAAGATTAAGAAGAACACTTTTGTCCGGAAATATTCCGACACCA 240 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTTGTCCGAAAGTTTTTGAAGAATCTTGTAG 242 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG 320 243 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG 323 301 GTTGTGGGTCACTTTGCTAAAGAATCAAGAAACAACCAGGGAACTTTTTAGTGGGAAAACAACTTTGTAG 323 324 GTTGTGGTCACTTTGCTGAAATGCAAGAGAAAACAACCAGGGAACTTTTTAGTGGTAAAAAAAA		601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660 [
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                                                                                                                1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG
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                              TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
                                              804 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
                                                                                              GTGACTGGTGGTGGGGGGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG
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Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Bllerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sashi
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Anderson, David W.
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Catterton, Elina
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93.7%; Score 1388.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR PELING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSequist version 0.1
LENGTH: 1870
                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (2)..(1870)
US-10-262-511-3
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US-10-791-666-3
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            APPLICANT: Shimets, Richard A. APPLICANT: Shimets, Richard A. APPLICANT: Shimets, Richard A. APPLICANT: Shimets, Richaele L. APPLICANT: Beach, Mark E. APPLICANT: Agee, Michaele L. APPLICANT: Agee, Michaele L. APPLICANT: Berghs, Constance C. RIVERNITOM: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511A
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-03
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PAPLICATION NUMBER: 60/321,917
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2001-10-09
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Pred. No. 0;
0; Mismatches
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
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Best Local Similarity 99.8%;
Matches 1390; Conservative
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; LOCATION: (2)
US-10-262-511A-3
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APPLICANT: With Manda, Maricar APPLICANT: With Maricar APPLICANT: Miranda, Maricar APPLICANT: Miranda, Maricar APPLICANT: Miranda, Maricar APPLICANT: Miranda, Maricar APPLICANT: Fiddle, Carl Johan TITLE OF INVENTION: Novel Hunan Kinases and Polynucleotides Encoding the Same FILE REFERENCE: LEX-0289-USA (2014) 10,666 CURRENT FILING DATE: 2004-03-02 PRIOR APPLICATION NUMBER: US/10/028,946 PRIOR APPLICATION NUMBER: US 60/258,335 PRIOR PILING DATE: 2000-12-27 NUMBER OF SEQ ID NOS: 4 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 6165
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Pred. No. 0;
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US-10-791-666-1
; Sequence 1, Application US/10791666
; GENERAL INFORMATION:
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             APPLICANT: Yu, Kuanchuan
APPLICANT: Wiranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
PRIOR PILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US/10/028,946
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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ORGANISM: homo sapiens
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GENERAL INFORMATION
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Pred. No. 0;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECT
FILE REFERENCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 7679
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Best Local Similarity 99.8
Matches 1390; Conservative
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ORGANISM: HUMAN
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                   ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7484498CB1
US-10-415-011-43
                       60/252,730
                                                           60/250,807
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/
PRIOR PILING DATE: 2000-11-25
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL PROGram
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.8%;
Matches 1390; Conservative
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ORGANISM: Homo sapiens
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	Sequence 3, Application US/1001/216 GENERAL INFORMATION: TITLE OF INVENTION: 13445, A Novel Human Myotonic Dystrophy Typ TITLE OF INVENTION: 13445, A Novel Human Myotonic Dystrophy Typ: TITLE OF INVENTION: Kinase and Uses Therefor TITLE OF INVENTION: WINBER: US/10/017,216 CURRENT APPLICATION NUMBER: US 60/242,429 FRICR APPLICATION NUMBER: US 60/242,429 FRICR FILING DATE: 2000-10-23 NUMBER: OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3 ILENGTH: 6159 TYPE: DNA ORGANISM: Homo sapiens US-10-017-216-3	Query Match 93.3%; Score 1381.8; DB 46; Length 6159; Best Local Similarity 99.5%; Pred. No. 0; 0. 0; Accession of the conservative or		131 181 191	Qy 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAAGGACTTCGAAGTCATGTAG	361	Qy 421 AAGAGGGAACATATTATCTCGAAGGACAACCCGTGGATCCCCCAATTACAGTATCCCT
121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTC	427 CINIGAMMENGARGAMGACITIANIGACCCCAGGACCCAGGACCCAGGACCCAGGACCCAGGACCCAGGACCCAGGACCCAGGACCCAGGACCCAGGACCCAGGACCCAGGACCCCAGGACCCCAGGACCCCAGGACCCCAGGACCCCAGGACCCCAGGACCCCAGGACCCCAGGACCCCAGGACCCCCAGGACCCCAGGACCCCCC	Qy 661 CTGAGAACATTCTCGFTGACGGCACACATCAAGCTGGTGGATTTTGGATCTGCCG 720 Db 727 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 786 Qy 721 CGAAAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780 Db 787 CGAAAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 846	781 TGGCTCCTGAAGTGCTGACTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT	907 GIGACTGGIGGICAGIGGGCGIGAITGCCIATGAGAIGAITTAIGGGAGAICCCCCTICG 901 CAGAGGAACCTCIGCCAGAACCTTCAATAACATTAIGAATTTCCAGCGGTTTTTGAAAT 111111111111111111111111111	QY 961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATTCAAAGCTTGTTGTGCG 1020 TTCCAGATGATGATGAGCAGTGACTTTCTTGATCTAAAGTTGTGTGCG 1086 Db 1027 TTCCAGAAAGAGAGAGAGTTTGAGAGGTTTTGCTGCTCTTTCTT	1081 ACTGGAACAATTCGTAACTCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG	OY 1141 ACACTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCCGTGCCAGC 1200

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Pred. No. 0;
0; Mismatches
FILE REFERENCE: MPIO1-294PIRNWOM
CURRENT APPLICATION NUMBER: PCT/USO2/41011
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/341,953
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 6162
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.5%;
Matches 1386; Conservative
                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)
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; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Slos-Santiago, Inmaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
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301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG 360 	361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420 	421 AAGAGGGAACATATTATCTCGAAGCACAGAGCCCGTGGATCCCCCAATTACAGTATGCCT 480 449 AAGAGGGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCT 508	481 TTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGACTTGCTGT 540	541 CACTITIGAATAGATATGAGGACCAGTIAGATGAAAACCTGATACAGTTTTACCTAGCTG 600	601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660	661 CTGAGAACAITCTCGTTGACCGCACGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720	721 CGAAATGAATTCAAACAGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780 	781 TGGCTCCTGAAGTGCTGACTGATGAACGGGGATGGAAAGGCACCTACGGCCTGGACT 840	841 GTGACTGGTGGTGGGGGGGTGATTGCCTATGACATGATTTATGGGAGATCCCCCTTCG 900	901 CACAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960 	961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1020 	1021 GCCAGAAAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTCTCTAAAATTG 1080 	1081 ACTGGAACAATTGGTAACTCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1140	1141 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200	1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACAGCAAGG 1260 1229 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACAGCAAGG 1288	1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTGGGTCTGGACTCCCCTGCCAAGA 1320	1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAGACTCTCAGGACA 1380 	1 AGTGTCACAAGGT 1393
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Qy 1081 ACTGGAACAACATTGGTAACTCTCCCCCCTTCGTTCCCACCTCAAGTCCGACGATG 1140 Db 1081 ACTGGAACAACATTGGTAACTCTCCCCCCTTCGTTTCCACGTCCAACAACAACATTGGTTCCTCCCCCTTCGTTCAACAACAACAACAACAACAACAAACA	1141 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 12	1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTAGGAAGG 126 1211 TGAGCCCTCAGGGTTTTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTAGGAAGG 127	SCCAAGA 	CTAGCTCCATGGAAAAGAAACTTCTCATCAAAGCAAAGAGGTACAAGAGCTCTCAGGACA 138	1381 AGTGTCACAAGGT 1393	SULT 14	Sequence 10, Application PC/TUS0241011 ; GENERAL INFORMATION: APPLICAMT: Millennime Pharmaceuticals, Inc	A AFPLICANT: ROBENTELY, INMEDIATED A THORS IN TREATING TIME OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207, TITTE OF INVENTION:	; IIILB CFINGWINCE: MPIO1-294PIRNWOM; CURRENT APPLICATION NUMBER: PCT/USO2/41011 ; CURRENT PILING DATE: 2002-12-19 ; CURRENT FILING DATE: 2002-12-19	FALOR FILING DATE: 2001-12-19; NUMBER OF SEQ ID NOS: 21; SOFTWARE: PARESEQ for Windows Version 4.0	; DENGTH: 6574 ; TYPE: DNA ; ORGANISM: Homo Sapiens PCT-US02-4/011-10	Query Match 93.3%; Score 1381.8; DB 1; Length 6574; Best Local Similarity 99.5%; Pred. No. 0; Matches 1386; Conservative 0: Mismatches 7: Indels 0: Gans 0:	Ascenderancemine	CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 1	121 CTCCTCTTTCCCGAGGGATATTAGATGCCTCTTTGTTCTTTGAAGAATGGTCTTTGTTCTTTTGAAGAATGCAGTCTTTGTTCTTTTGAAGAATGCAGTCTTTGTTCTTTTGAAGAATGCAGTCTTTGTTCTTTTGAAGAATGCAGTCTTTGTTCTTTTGAAGAATGCAGTCTTTGTTCTTTTGAAGAATGCAGTCTTTGTTTTGAAGAATGCAGTCTTTGTTTTTAGAATTTTGAAGAAGAAGAAGAATGAAGAAG	181 AGCTGCTCTGAAGATTAAGCACGTGAGCAACTTTGTCCGAAGTATCCGACACCACACACA	241 TAGCTGAGTTACAGGGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 3	Db 269 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 328

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GENERAL INFORMATION:
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Publication No. US20040091993A1

GENERAL INFORMATION:

APPLICANT: WESTER, Marion et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOOL164DIV II

CURRENT FILING DATE: 2003-12-02

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PASLESEQ for Windows Version 4.0

SEQ ID NO 1
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CB1
US-10-311-034-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.7%; Score 1476.2; Best Local Similarity 99.8%; Pred. No. 0; Matches 1478; Conservative 0; Mismatches
HE, Ann
THORNTON, Michael
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 2066
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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DB 17; Length 2066;
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Sequence 33, Application US/10311034
Publication No. US20040023242A1
GENERAL INFORMATION:
APPLICANT: TNCYTE GENOMICS, INC.
APPLICANT: ILAL, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Clga
APPLICANT: AU-YOUNG, Janice
APPLICANT: AU-YOUNG, Janice
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: TRIBOULEY, CATHERING A.
APPLICANT: GANDMI, SAFA R.
APPLICANT: GANDMI, SAFA R.
APPLICANT: GREENWALD, SAFA R.

GANDHI, Ameena R.
TRIBOULEY, Catherine M.
CHAWLA, Narinder K.
YAO, Nonique G.
LU, Dyung Aina M.
GREENWALD, Sara R.
RAMKUMAR, Jayalaxmi

NGUYEN, Danniel B. TANG, Y. Tom Neil

APPLICANT: APPLICANT:

BURFORD, KEARNEY

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Ju, Jingfang
Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
                                                                                                                  Ellerman, Karen
Malyankar, Uriel M.
                                                                                                                                                    Gorman, Linda
Zerhusen, Bryan D.
Anderson, David W.
              Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
                                                                                                                                                                                       Zhong, Mei
Catterton, Elina
                                                                                                                                         Ort, Tatiana
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ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: (2)..(1870)
US-10-262-511-3
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APPLICANT:
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CACTITIGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 623
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APPLICANT: 31, Gatterion, Lilia APPLICANT: Rail Gatterion, Carol E. APPLICANT: Research: Carol E. APPLICANT: Research: Carol E. APPLICANT: Research: Martin G. APPLICANT: Receiver, G. 2003-05-28 G. CURRENT FILING DATE: 2001-10-02 G. CURRENT FILING DATE: 2001-10-02 G. CURRENT FILING DATE: 2001-01-02 G. CURRENT FILING DATE: 2001-01-02 G. CURRENT FILING DATE: 2001-01-02 G. CURRENT FILING DATE: 2001-01-03 G. CORRENT G. CORRENT
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US-10-262-511-3; Sequence 3, Application US/10262511; Publication No. US20040038223A1; GENERAL INFORMATION:

Same

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| Publication No. US20040209297A1
| GENERAL INFORMATION:
| APPLICANT: Wi, Xuanchuan
| APPLICANT: Wi, Xuanchuan
| APPLICANT: Wi, Xuanchuan
| APPLICANT: Fridale, Carl Johan
| TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
| FILE REFERENCE: LEX-0229-US
| CURRENT APPLICATION NUMBER: US/10/791,666
| CURRENT APPLICATION NUMBER: US/10/028,946
| PRIOR PILING DATE: 2001-12-20
| PRIOR PILING DATE: 2001-12-20
| PRIOR FILING DATE: 2001-12-27
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: FasteSEQ for Windows Version 4.0
| SEQ ID NO 3
| LENGTH: 5877
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0; Mismatches
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Matches 1390, Conservative
                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: homo sapiens
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        TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG
                                         TCAAATATGGAGCGCGGAATCCTTTGGATGCTGCTGCTGCTGAACCCATTGCCAGCCGGG
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; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CB1
US-10-415-011-43
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93.7%; Score 1388.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches
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TITLE OF INVENTION: HUMAN KINASES
FILE REPERENCE: PL-0262 USN
CURRENT FILIDED DATE: 2003-04-18
FRICH APPLICATION NUMBER: US/10/415,011
CURRENT FILING DATE: 2001-10-20
PRIOR PILING DATE: 2001-10-20
PRIOR PLING DATE: 2001-10-20
PRIOR PLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,410
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-11-03
PRIOR PLING DATE: 2000-11-03
PRIOR PLING DATE: 2000-11-09
PRIOR PLING DATE: 2000-11-09
PRIOR PLING DATE: 2000-11-09
PRIOR PLING DATE: 2000-11-16
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-32
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HAFALIA, April J.A.
NGUYEN, Danniel B.
GANDHI, Ameena R.
LU, Yan
YUE, Henry
BURFORD, Neil
BANDMAN, Olga
TRIBOULEY, Catherine M.
LAL, Preeti G.
RECIPON, Shirley A.
LU, Dyung Aina M.
BOROWSKY, Mark L.
HORNYDN, Michael B.
                                                                                                                                                                                            Sequence 43, Application US/10415011
Publication No. US20040053394A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        APPLICANT: INCYTE CORPORATION
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: BAUGHN, Mariah R.
APPLICANT: CHAWLA, Nariader K.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: XU, Yuning
APPLICANT: ARVIZU, Chandra S.
APPLICANT: YAO, MONIQUE G.
APPLICANT: YAO, MONIQUE G.
APPLICANT: RAMKUMAR, Jayalaxmi
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THANGAVELU, Kavitha
KHAN, Farrah A.
ISON, Craig H.
1381 AGTGTCACAAGGT 1393
                                                 AĞTĞTCACAAGAT 1403
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ORGANISM: Homo sapiens
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W3-10-017-216-1

Sequence 1, Application US/10017216

Publication No. US2020160483A1

Sequence 1, Application No. US2020160483A1

GENERAL INFORMATION:

APPLICANT: KAPELLER-LIBERMANN, Rosana

TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Proti

TITLE OF INVENTION: Kinase and Uses Therefor

TITLE OF INVENTION: US-57U1

CURRENT PILING DATE: 2001-10-23

PRIOR FILING DATE: 2001-10-23

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 6574

TYPE: DNA
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511 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670
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                                                        CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCCGATTGGGACCCCAGATTACA
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                                  CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG
                                                                                                                CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCCAGATTACA
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                            Sequence 11, Application US/10325430

Sequence 11, Application US 20030153525A1

Bublication No. US20030153525A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Rosenfield, Julia Bath

TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING

TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,

TITLE OF INVENTION: 3289,336 and 52908

FILE REFERENCE: MPI01-294PIRNM

CURRENT FILING DATE: 2002-12-19

PRIOR PLILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 21

SSOFTWARE: PSEASEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 6162
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.5%;
Matches 1386; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)...(6162)
US-10-325-430-11
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| Sequence 10, Application US/10325430
| Publication No. US200301535251
| Shakati Involvation
| APPLICANT: Millennium Pharmaceuticals, Inc
| APPLICANT: Rosenfeld, Julie Beth
| TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
| TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
| TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
| TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
| TITLE OF INVENTION: PAIN NAMER: US/10/325, 430
| CURRENT APPLICATION NUMBER: US 60/341,953
| PRIOR APPLICATION NUMBER: US 60/341,953
| PRIOR PILING DATE: 2001-12-19
| NUMBER OF SEQ ID NOS: 21
| SOFTWARE: FeatSEQ for Windows Version 4.0
| SEQ ID NO 10
| LENGTH: 6574
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Pred. No. 0;
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Best Local Similarity 99.5%;
Matches 1386; Conservative (
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ORGANISM: Homo Sapiens
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                                                   DB 13;
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Pred. No. 0;
0; Mismatches
                                                Query Match 93.3%;
Best Local Similarity 99.5%;
Matches 1386; Conservative
ORGANISM: Homo sapiens
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US-10-017-216-1
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                                                                                            AGTGTCACAAGGT
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; LOCATION: (19)...(6180)
US-10-757-262-51
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                              TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
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È	1261	1261 CACTGGGGATTCTTGGTAGATCTGTTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA	1320
Db	1289 (CACTGGGGATTCTTGGTAGATCTGATTGTGTTGTCGGGTCTGGACTCCCCTGCCAAGA	1348
ò	1321	1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGGCTACAAGACTCTCAGGACA	1380
Db	1349 (1349 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGGACTCTCAGGACA	1408
ò	1381	1381 AGTGTCACAAGGT 1393	
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Search completed: March 19, 2005, 18:10:57 Job time : 813.2 sec8

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Sequence 10, Appl Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 15, Appli Sequence 15, Appli Sequence 6, Appli Sequence 11, Appli Sequence 11, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 11, Appli		NUCLEIC KINASE PROTEINS, AND USES	Length 1515; Indels 0; Gaps 0;	ACCCATTGCCAACCGGG 60	TGACTCAACAGCAGATGT 120	CTTTGAAGAATGCAGTC 180 	GGAAGTATTCCGACACCA 240	AGTCAGAAGTCTTGTAG 300 AGTCAGAAGTCTTGTAG 316	CAACCGGGACATCTATG 360 AACCGGGGACATCTATG 376
US-08-422-699A-10 US-08-422-706B-10 US-09-442-100-7 US-09-393-106-7 US-09-509-902A-6 US-09-509-902A-15 US-09-509-902A-15 US-09-509-902A-15 US-09-513-857-2 US-08-860-150-6 US-09-318-132-6 US-09-318-132-6 US-09-318-132-6 US-09-272-796-11 US-09-442-100-5 US-09-2442-100-5 US-09-2442-100-5 US-09-2482-100-5 US-09-2482-100-5 US-09-2482-100-5 US-09-2482-100-5 US-09-2482-100-5 US-09-2482-100-5 US-09-2482-100-1	ALIGNMENTS	KINASE PROTEINS, ENCODING HUMAN F 04,471A on 4.0	; Score 1481; DB 4; ; Pred. No. 0; 0; Mismatches 0;	TCAAATATGGAGCGCGGAATCCTTTGGATGCTGCTGCTGCTGAACCCATTGCCAACCGG 	CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 	CTCCTCTTTCCCGAGAAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 	agcctgctctgatgaagattaagcacgtgagcaactttgtccggaagtattccgacacca 	TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTA 	GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG
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Sequence 1, Application US/10238709
Patent No. 6680188
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERBNCE: CL0001164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARR: FRSISEQ for Windows Version 4.0
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US-10-238-709-1
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                                        Score 1388.2;
                                                     Pred. No. 0;
0; Mismatches
                                     Query Match 93.7%;
Best Local Similarity 99.8%;
Matches 1390; Conservative
; ORGANISM: homo sapiens
US-10-028-946-3
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                                                                TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
IENGTH: 5877
TYPE: DNA
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Sequence 1, Application US/09916204

Patent No. 6638745

GENERAL INFORMATION:

APPLICANT: WEI, MING-Hui et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: CLOOIL64CIP

CURRENT APPLICATION NUMBER: US/09/916,204

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
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    734 CTATGAAAGTGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTAAGG 793
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                                                                              794 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCT
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Pred. No. 2.2e-241;
0; Mismatches 2;
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Best Local Similarity 99.7%;
Matches 746; Conservative
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ORGANISM: Human
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APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje T.
TILLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE REFERENCE: 802
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SEQ ID NO 419
SEQ ID NO 419
                                                                                                                                                                                             Sequence 419, Application US/09774528 Patent No. 6743619
                                                                              Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
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Matches 949; Conservative
                                                          AGTGTCACAAGGT
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, LOCATION: (364)..(2010)
US-09-774-528-419
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APPLICANT: Tang, Y.
APPLICANT: Shou, Pin
APPLICANT: Goodrich,
APPLICANT: Liu, Chen
APPLICANT: Asundi, I
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US-09-949-016-2640

i Sequence 2640, Application US/09949016

j Patent No. 6812339

j Patent No. 6812339

j TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERRING: CLO01307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-06-08

PRIOR FILING DATE: 2000-06

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0
                                                                                                                         244 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 303
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   CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 183
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US-09-949-016-2640
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Patent No. 6692948
TITLE OF INVENTION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITILE OF INVENTION: THEREOF
FILE REPERBACE: CLOO1164CIP-DIV
CURRENT APPLICATION NUMBER: US/10/282,048
NUMBER OF SEQ ID NOS: 6
SOPTWARE: PESTSO for Windows Version 4.0
SEQ ID NO
                                                                                                                                                                                               GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAAGCAACCGGGGACATCTATG
                                                                                                                                                                                                                                        CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCCAGGAGCAGGTTTCATTTTTGAGG
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                                 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA
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46; Conservative
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APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen J.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                    2098 criccaritricing coarcing coartricing carata
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NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5830A2

TELECOMUNICATION INFORMATION:
TELEPAN: 617-861-9640

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
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PRICATION APPLICATION DATA:
PRICATION NUMBER: US 08/023,612
PRICA APPLICATION DATA:
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
PRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
PRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
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APPLICATION NUMBER: PCT/GB93/00253
PRICA APPLICATION NUMBER: BCT/GB93/00253
PRICA APPLICATION NUMBER: GB9202485.0
PRILING DATE: 05-FEB-1993
APPLICATION NUMBER: GB9202485.0
PRILING DATE: 06-FEB-1993
APPLICATION NUMBER: GB9202485.0
PRILING DATE: 06-PEB-1993
APPLICATION NUMBER: GB9202485.0
                                                       1210 CAGGCTTCTCGGGTGAAGAACTGCCGTT
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                                                                                                                                                                                                                                 Sequence 12, Application US/08422699A Patent No. 5955265 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTED:
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 54.0
Matches 534; Conservative
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STRANDEDNESS: double
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CLASSIFICATION:
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     Pred. No. 4.3e-68;
0; Mismatches 519; Indels
52.5%;
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Matches 591; Conservative
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Brook, J. David
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Sequence 12, Application US/08422706B Patent No. 5977333

RESULT 10 US-08-422-706B-12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 GTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGGAAAGCAACCGGGGACATCTATGCTA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 ccanacridecccadeacanatracerdeccentricriecagregecegageccardede
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAG
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APPLICANT: Bousman, David B.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 225.6; DB 2;
Pred. No. 5.3e-65;
0; Mismatches 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 08-AUG-1994

PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612

PRICA PAPLICATION DATA:
APPLICATION NUMBER: US 07/839,255

PRICA PAPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545

PRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545

PRICA APPLICATION NUMBER: PCT/US93/01545

PRICA APPLICATION NUMBER: PCT/US93/00253

PRICATION NUMBER: PCT/US93/00253

PRICATION NUMBER: PCT/US93/00253

PRILING DATE: 05-FEB-1993

PRICATION NUMBER: PCT/US93/00253

PRILING DATE: 05-FEB-1993
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REGISTRATION NUMBER: 32,227
REPERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION:
TELECOMMUNICATION: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
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APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ilarity 54.0%;
Conservative (
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FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                         Massachusetts
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 534; Conserva
                                                                                                                                                                                                                               CITY: Lexington STATE: Marring
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                                                                                                                                                                 ZIP: 02713

COMPUTER READABLE FORM:
MEDIUM TREE Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN ROLEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
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Pred. No. 1e-62;
0; Mismatches 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: G1922
ATTORNEY, AGENT INFORMATION:
NAME: Granahan, Particia
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION NUMBER: 32,227
TELECOMMUNICATION NUMBER: 32,227
TELECOMMUNICATION NUMBER: 31,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
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MOLECULE TYPE: DNA (genomic)
Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5%;
Matches 511; Conservative
                                        CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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LOCATION:
US-08-422-699A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1069 TCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCCACCCTCA 1128
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                                                                                                                    423 rdaagarcardaacaagreceacarecreaagageceaegerererererereres 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGATGAGAACTACCTGTACCTGGTCATGGAGTATTACGTGGGCGGGGACCTGCTGACAC 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603 TGCTGAGCAAGTTTGGGGAGCGGATTCCGGCCGAGATGGCGCGCGTTCTACCTGGCGGAGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCGCGA 723
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                                        TGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGGAAG
                                                                                                                                                                                                                                                                                               AGAGGGACGTGTTGGTGAATGGGGACCGGCGCTGGATCACGCAGCTGCACTTCGCCTTCC
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APPLICANT: Brook, J. David

APPLICANT: Housan, David E.

APPLICANT: Harley, Helen G.

APPLICANT: Harley, Helen G.

APPLICANT: Johnson, Keith J.

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC

TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
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Patent No. 5955265
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CORRESPONDENCE ADDRESS:
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; LOCATION:
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APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Reith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith & Reynolds, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08422706B; Patent No. 5977333; GENERAL INFORMATION: APPLICANT: HOUSMAN, David APPLICANT: Housman, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Hamilton, Brook,
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STATE: Massachusetts
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US-08-422-706B-8
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234 GACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGT 293
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Pred. No. 1e-62;
0; Mismatches 412;
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REGISTRATION NUMBER: 32,227
REFERNICE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
RHOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB92(
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5%;
Matches 511; Conservative
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INFORMATION FOR SEQ ID NO:
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LENGTH: 2511 base pair
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                                                                                                                                                                                                                                                                                                                              236 CACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                   296 TGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 GCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAAACCTGATACAGTTTTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    596 AGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCCAGGAGCAGGTTTCATTTTT
                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                          Length 3182;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                          Score 218.4; DB 1;
Pred. No. 1.6e-62;
0; Mismatches 411;
                                                   Ξ
                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.5%;
Matches 510; Conservative
                        TELEX: 762829
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
      713/651-5246
                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                  US-08-484-044-11
        TELEFAX:
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                                                                  TCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAAACTCCCGATTGGGACCCCCA
                                                                                                        GATTACATGCCTCCTGA----AGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTAC
                                                                                                                                                                                                                                          GGCCTGGACTGTGACTGGTGAGTGGGCGTGATTGCCCTATGAGATGTTTATGCGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
APPLICANT: Fu, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Pizzuti, Antonio
APPLICANT: Penwick, Raymond G.
APPLICANT: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1008 AGCTTGTTGTGCGCCAGAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC
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ZIP: 77010-3095
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019,940
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fulbright & Jaworski, 1
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: D-5443
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08484044
Patent No. 5552282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Houston
STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-484-044-11
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; OTHER INFORMATION: n = A,T,C or G US-10-238-709-3
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Patent No. 6680188

Patent No. 6680188

AEPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILE NOS: 4
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: TREREOF
FILE REFERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FARTSEQ for Windows Version 4.0
         1583 TCCCTTCTTCTTTGGCCTCGACTGGGATGGTCTCCGGGACAGCGTGCCCCCCTTTACACC 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            803 GATGAACGGGGATGGAAAAGGCACCTACGCCTGGACTGTGACTGGTGGTCAGTGGGCGT
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                                                    1121 CACCCTCAAGTCCGACGATGACACCTCCAATTTTGA 1156
                                                                                               1643 GGATTTCGAAGGTGCCACCGACATGCAACTTCGA 1678
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                                                                                                                                                                                                               Sequence 3, Application US/09804471A Patent No. 6479269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1)...(174493)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0
Matches 205; Conservative
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NAME/KEY: misc_feature
LOCATION: (1)...(174493)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 174493
TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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US-09-804-471A-3
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                                                                                                                                                                                                                                                                                                     863 GATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAAC
                                                    Gaps
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0
  Length 174493;
                                                                                                   743 GGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGGCTCCTGAA
                                                 Indels
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Score 205; DB 4;
Pred. No. 1e-56;
Query Match 13.8%; Score 205; DE Best Local Similarity 100.0%; Pred. No. 1e-Matches 205; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         CTTCAATAACATTATGAATTTCCAG 947
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Job time : 264.498 secs
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March 19, 2005, 07:45:41; Search time 4489.47 Seconds (without alignments) 12556.766 Million cell updates/sec
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1481
1 tcaaatatggagcgggaat.....cccgggggccgctgctggctc 1481
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                         34239544 seqs, 19032134700 residues
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                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                , OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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995-9881::
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BP146990 BP146990	BM904785 AGENCOURT	CR746615 CR746615	BG808196 2082-86 M	BG944539 ax51f11.x	CR746792 CR746792	BQ417810 ik51b06.y	CN682405 E0164B04-	CN678533 E0112C12-	BF562826 UI-R-BJ0p	BI654262 603280370	CG501399 OST45249	CG501400 OST45250	CG652891 OST417039	BF380737 IL2-UT007	BF344814 602014091	BX516291 BX516291	AI882189 ul31e08.y	CC325092 XL068 Bay	AW525215 UI-R-BJ0p	CG869028 AB0155 Sa	BF932611 RC5-NT018	BF763211 IL2-CS004	CK841805 UI-R-BJ0p
SUMMARIES	ID	BP146990	BM904785	CR746615	BG808196	BG944539	CR746792	BQ417810	CN682405	CN678533	BF562826	BI654262	CG501399	CG501400	CG652891	BF380737	BF344814	BX516291	AI882189	CC325092	AW525215	CG869028	BF932611	BF763211	CK841805
	DB	2	Ŋ	7	4	4	7	2	7	7	~	4	σ	σ	σ	7	~	Ŋ	-	0	7	σ	N	7	7
	Query Match Length	698	1085	492	909	427	485	617	481	479	490	821	449	450	512	340	423	582	521	355	539	336	321	335	524
46	Query Match	40.7	35.2	32.3	29.6	28.6	27.6	27.0	25.7	25.5	22.8	22.3	22.1	21.9	21.5	21.2	21.1	21.1	19.0	19.0	18.8	18.4	18.3	17.7	17.7
	Score	602.6	521.2	478	438.4	423.8	409.4	400.4	380	378	337	329.8	327	325	318.2	314.2	312.8	312.6	281.6	281.4	278.8	272.6	270.8	262.4	262.4
	Result No.		7	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	c 15	16	17	18	19	c 50	21	c 55	23	c 24

Length 698;

40.7%; Score 602.6; DB 5; 91.4%; Pred. No. 7.9e-172;

Query Match Best Local Similarity

6 325 3 BC008127 BC008127 BBB27314 6 38 9 CG65761 CG65761 CG7426725 6 54 7 CF744826 CF744826 DR3-10117 6 54 7 CF744826 CF744826 UL M-GV0- 6 647 7 CF744826 UL M-GV0- 1 268 3 BC02044 BC002044 BC00- 1 268 3 BC056615 BC024150 BC024150 BC024150 0 398 3 BC056615 BC024150 BC024150 BC024150 0 2862 3 BC056615 BC024150 BC024150 BC024150 0 2862 3 BC056615 BC024150 BC024100 BC024100 BC024100 BC02410	ALIGNMENTS	BP146990 BP146900 BP14600 B	ovary"
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1. .1085
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Rom"
// Organism="Rom"
// Dasoue rype="melanotic melanoma"
// Lab host="DH10B" (phage-resistant)"
// Lab host="DH10B" (phage-resistant)"
// Loo = 11b="NH1 MGC 72"
// Anote="Organ: Skin; Vector: pcWV-SPORT6; Site_1: Not1;
// Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
Technologies."
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CR746615 NIH MGC 72 Homo sapiens cDNA clone IMAGp998D0712279;
IMAGE:5557590 5', mRNA sequence.
CR746615.1 GI:51659741
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Homo sapiens
Eukarycia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov
Plate: LLAM12279 row: d column: 07
High quality sequence stop: 510.
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1 (Dases 1 to 1085)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                              CAGGAGCAGGTTTCATTTTTGAGGAAGAACAGAACATCTTATCCCGGAGCACAACCCT
                                                                                                                    TGGATCCCCCAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAA
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                                        CAGGAGCAGGTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCG
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
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    60; Indels
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    638; Conservative
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BG808196
2082-86 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
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| forganism="Mus musculus"
| forganism="MRNA"
| mol type="neuval retina"
| tissue type="neuval retina"
| dev stage="embryonic day 14.5 post-fertilization"
| clone_lib="Mouse E14.5 retina lambda ZAP II Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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86.4%; Pred. No. 9.7e-122;
ive 0; Mismatches 76;
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                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                    BG808196.1 GI:17955172
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      485 CATGGAAA 492
                                                                                                                                                       mRNA sequence.
BG808196
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Matches 484; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"

db_xref="taxon:9606"

/db_xref="taxon:9606"

/clone="INAGP99B0012279; IMAGE:5557590"

/tissue type="melanotic melanoma"

/lab host="DH10B (phage=resistant)"

/clone=lib="NIH MGC_72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: Not1;

Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 TGACCCCCAAAGTGAGCAGTGACTTTCTTGATTCTAAAGCTTGTTGTGCGGCCAGAA 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 CAATTTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCC 364
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                    Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E. Peters, M., Radelof, U. and Schneider, D. I.M. A.G.E. CDNA Clone Collection Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.3%; Score 478; DB 7; Length 492; 98.6%; Pred. No. 7.3e-134; Live 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
    (bases 1 to 492)
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Matches 481; Conservative
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Query Match 28.6%;
Best Local Similarity 99.5%;
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                                                                                                                                                                                            BG944539 427 bp mRNA linear EST 15-JAN-2003 ax51f11.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library) Homo sapiens cDNA clone ax51f11 random, mRNA sequence.
                               540
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primatee; Catarrhini; Hominidae; Homo. 1 (bases 1 to 427)
Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
Gene expression in proliferating human erythroid cells Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Jeffery L. Miller
Laboratory of Chemical Blology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9817, National Institutes of Health, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fel: 301 402 2373

Tel: 301 402 2373

Fel: 301 435 5148

Email: jm/fenin.gov

DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).

Plate: 51 row: f column: 11

Seq primer: -21M13 forward primer (ABI).

Location/Qualifiers
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461 AGGAGAAGAACATATTATCTCGGAGCACGAGTCCTTGGATCCCCCAGTTACAGTACGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.nisc.nih.gov/)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                        541 CACTTTTGAATAGATATGAG 560
                                                                                                          581 CGCTTCTGAACAGATACGAG 600
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                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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CR746792 CT746792 485 bp mRNA linear EST 30-AUG-2004
CR746792 NCI CGAP Brn64 Homo sapiens CDNA clone IMACp998B239412 ;
IMAGE:4149886 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                 311
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                                                                                                                                                                                                                                                                                                                                                                                                    371
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1 (Dases I to 485)

Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E., Peters, M., Radelof, U. and Schneider, D.

I.M.A.G.E. cDNA Clone Collection

Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (cloneerzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                181 TITGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTG
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                                                                                                                                                1 ccaccacacatarracarcccrcrrrcrrcrrrcaacaatacacacrccrccrc
                                                                                                                                                                                                  192 ATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACACATAGCTGAGTTA
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                                                 Gaps
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SZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
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RZPDIIB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Arlart
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
www.rzpd.de
                                              Indels
DB 4;
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Score 423.8; DB 4.
Pred. No. 2.4e-117
0; Mismatches 2.
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/mol_type="mRNA"
/mol_type="mRNA"
/dev stage="mRNA"
/dev stage="p.c. 14.5"
/dev stage="p.c. 14.5"
/dev stage="p.c. 14.5"
/lab_host="E. coil-1bH128 (GIBCO)"
/clone_lib="Kaestner ngn3 wt"
/lab_host="E. coil-1bH128 (GIBCO)"
/clone_lib="Kaestner ngn3 wt"
/note="forgan: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
Not I; Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The CDNA's were prepared with an oligo containing a
NotI site, and Sall linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-Sall sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/-. The wt library is in
-coopert T7 promoter is 5'."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 AACCCGCCCTGATGAAGATGAAGCACGTGAGCAGCTTTGTCCAGAAGTATTCCGACACA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Scearce (mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360
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86.0%; Pred. No. 3.9e-110;
iive 0; Mismatches 72;
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                                                                                                                                                                                                                                                      organism="Mus musculus"
          Email: dmelton@biohp.harvard.edu
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Matches 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
AA 02138
Tel: 617-495-1812
Fax: 617-495-8557
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 617)
/db_xref="taxon:9606"
/clone="IMAGD998E329412; IMAGE:4149886"
/tissue_type="glioblastoma with EGFR amplification"
/lab host="milloB (Ti phage-resistant)"
/clone_lib="NCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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ik51b06.yl Kaestner ngn3 wt Mus musculus cDNA 5' similar to
TR:088937 088937 RHO/RAC-INTERACTING CITRON KINASE SHORT ISOFORM.
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Unpublished (2000)
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                                                                                                                                                                                                                                                                       Query Match 27.6%; Score 409.4; DB 7; Length 485; Best Local Similarity 99.8%; Pred. No. 6.3e-113; Matches 410; Conservative 0; Mismatches 1; Indels 0
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Sharov,A.A., Plao,Y., Matoba,R., Dudekula,D.B., Qian,Y., VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C., VanBuren,V., Falco,G., Hamatani,T., Alba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kinber,M.L., Yoshikawa,T., Jazadat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L., Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A., Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A., D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.

Transcriptome analysis of mouse stem cells and early embryos Contact: Dawood B. Dudekula
E0164B04-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04 IMAGE:30782511 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Genetics
National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0164 row: B column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="niaEST:E0164B04-5"
|db_xref="taxon:10090"
|clone="NIA:E0164B04 IMAGE:30782511"

    .481
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="129Sv/EvTac"

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POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                    Mus musculus (house mouse)
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CN682405.1 GI:47448856
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ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. B. 1 (bases 1 to 479)

Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y., VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey, U.C., Tanaka,T.S., Kimber, W.L., Yoshikawa,T., Akutsu,H., Sharova,L., Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Abardat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L., Schlesinger,D., Keller,J., Konath,T., Hogan,B.L., Curci,A., Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A., D'Urso,M., Kelso,J., Hide,W. and Ko,M.S Transcriptone analysis of mouse stem cells and early embryos PloS Biol. 1 (3), 410-419 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GATCCAGITITACCITGCTGAGCTGATTTTGGCTGTCCACAGCGTGCACCAGATGGGATA 360
                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                 461 CCCCCAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCCCCAGTTACAGTACGCCTTTCAGGACAAAAAAAAACCTTTACCTGGTCATGGAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GCCTGGAGGGGATTTGCTGTCGCTTCTGAACAGATACGAGGACCAATTAGATGAGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 CGAAGTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAA
                                                                                                                                                                                          1 CGAAGTTCGAAGCCTTGTGGGCTGTGGTCACTTCGCTGAAGTGCAGGTGGTTAGAGAGAA
                                                                                                                                                                                                                                                       341 AGCAACCGGGGACATCTATGCTATGAAAGTGAAGAAGAAGAAGGCTTTATTGGCCCAGGA
                                                                                                                                                                                                                                                                                                                                                                              401 GCAGGITICATITITIGAGGAAGAGGGGAACATAITAICICGGAAGCACAAGCCCGTGGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            521 GCCTGGAGGGGACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      581 GATACAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 CGTGCATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 rerecarceacarcarcasecceasaacarcercercarceaceaceacacarcarcaaecr
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                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: E0112 row: C column: 12 Seq primer: M13 Reverse High quality sequence stop: 479
                                                                   3;
Length 481
                                                                Indels
   Score 380; DB 7; L
Pred. No. 5.9e-104;
0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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CN678533.1 GI:47444984
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Query Match 25.7%;
Best Local Similarity 88.0%;
Matches 426; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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/ db xref="tradgue-Dawley"
/ db xref="tradgue-Dawley"
/ clone="UI-R-BJ0p-aip-b-06-0-UI"
/ dev stage="adult"
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/ lab_host="DH108 [Life Technologies]"
/ clone=lib="UI-R-BJ0p"
/ clone=lib="UI-R-BJ0p"
/ clone=lib="UI-R-BJ0p"
/ note="Vector: pT773b-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I: Site_2: Eco RI; The UI-R-BJ0p
library is a subtracted library derived from the UI-R-AB1,
UI-R-AB1, UI-R-AD1, UI-R-AB1, UI-R-AB1, and
UI-R-AB1, UI-R-AB1, UI-R-AB1, and
UI-R-AB1, UI-R-AB1, UI-R-AB1, and
UI-R-AB1, UI-R-AB1, UI-R-AB1, uI-R-AB1, and
UI-R-AB1, UI-R-AB1, UI-R-AB1, uI-R-AB1, uI-R-AB1, and
UI-R-AB1, uI-R-AB1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9265
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@inage.llnl.gov). IMAGE ID= 1797673
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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760
                                                                                                                           421 GGTGGATTTTGGATCAGCCGCTAAGATGAATTCAAATAA---GGTGGATGCCAAACTCCC 477
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                                                                                                                                                                                                                                                                                                                                                                                                                  BF562826
UI-R-BJOp-aip-b-06-0-UI.rl UI-R-BJOp Rattus norvegicus cDNA clone
UI-R-BJOp-aip-b-06-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 490)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                         701 GGTGGATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF562826
BF562826.1 GI:11672556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
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Best Local Similarity 85.3%
Matches 376; Conservative
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PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                             RESULT 10
BF562826
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTGGAGGGGACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCT 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581 GATACAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATA 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 CGTGCATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 AGCAACCGGGGACATCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGA
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                                                                                                                  /mol_type="mRNA"
/strain=1129Sv/EvTac"
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/cell line="129.3 ES cells"
/lab_host="DH108"
                                                                                      organism="Mus musculus"
                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 424; Conservative
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Best Local Similarity
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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 449)

S. (bases 1.0. 449)
S. Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huangy, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qann, N., Sahw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.
Whk! kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Contect: Zambrowicz BP
OmniBank
             Library constructed by Life Technologies. Investigators providing samples: Lothar Hennishausen/Priscilla Purth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG501399 449 bp mRNA linear GSS 01-OCT-2003 OST45249 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST45249,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 AACCCGCCCTGATGAAGATGAAGCACGTGAGCAGCTTAGTCCAGAAGTATTCCGACACA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 ATGCTATGAAAGTGATGA-AGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477 ATGCCATGAAAATCATGACAGAAGAAGACTTTGCTGGCCCCAGGAACAGGTTTCATTTTTT 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 GAGGAAGAGGGGAA-CATATTATCTCGAAGCACAAGCCCGGGATCCCCCAATTACAGTA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 CGCCTTTCAGGACCAAAAATAAACTTTACCTGGTCATGGACACTATCAGCCTGGATGGG 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG
                                                                                                                                                                                                                                                                                                                                                                                                   117 TCAAGTATGGTGTGCGGAACCCGCCGGAGGCCAGTGCCTCCGAGCCCATTGCCAGTCGGG
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                                                                                                                                                                                                      Length 821;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                   22.3%; Score 329.8; DB 4;
84.2%; Pred. No. 1.5e-88;
ive 0; Mismatches 77;
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                                                                                                     CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCTTTATGACTCAACAGCAGATGT 120
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
I (bases 1 to 81)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1990)
CTCCAGGCTAAATCTCTTCTTCCAGGGAAACCGCCCTCATGACTCAACAGAGAGTGT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llhl.gov
Plate: LLAM1786 row: 1 column: 17
High quality sequence stop: 648.
                                                                                                                                                                                                                                 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTTGAAGAATGCAGTC
                                                                                                                                                                                                                                                                                                                                                           AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
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/dev_stage="5 months"
/lab_host="DH108"
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/organism="Mus musculus"
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/clone="IMAGE:5310496"
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/strain="NMRI"
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Class: Gene Trap.
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Zambrowicz.B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BaltrandelRio,H., Buxton,B.C., Edwards,J., Finch,R.A., Kappier,J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohhhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
Whal kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Contact: Zambrowicz BP
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                        Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9,392(6676):608-11) Class: Gene Trap.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                    Gaps
1000 Research Forest Drive, The Woodlands, TX 77381, USA
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                                                                                                                                                                                                                                                       Length 449;
                                                                                                                                                                                                                                                                                   31; Indels
                                                                                                                                                      /db xref="taxon:10090"
/clone="0ST45249"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                   ch 22.1%; Score 327; DB 9; al Similarity 91.8%; Pred. No. 8.6e-88; 345; Conservative 0; Mismatches 31;
                                                                                                           /organism="Mus musculus"
                                                                                                                         /mol_type="mRNA"
/strain="129Sv/Ev"
                Email: materials@lexgen.com
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OST417039 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST417039,
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
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Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Guptea, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Rey, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Mukl Kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AGCTGCCGTTTGTGGGATTTTCGTACAGCAAGGCACTGGGGGTATCTTGGTAGATCTGAGT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.9%; Score 325; DB 9; Length 45
Best Local Similarity 91.7%; Pred. No. 3.5e-87;
Matches 343; Conservative 0; Mismatches 31; Indele
                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                1. .450
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                                                                                                                                                                                                        Location/Qualifiers
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Mus musculus
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Query Match 21.2%;
Best Local Similarity 97.6%;
Matches 319; Conservative
                                     10737800
                                                                                                                        Brazil
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JOURNAL MEDLINE PUBMED COMMENT
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(bases 1 to 340)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Solaman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Warstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Here,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                               Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Bemail: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
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   Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                     Score 318.2; DB 9; Length 512;
Pred. No. 4.4e-85;
0; Mismatches 29; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 bp mRNA linear IL2-UT0073-170900-167-H01 UT0073 Homo sapiens CDNA, BF380737
                                                                                                                                                                                                                                                                        /cell_type="embryonic stem cell"
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Location/Qualifiers
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                 Contact: Zambrowicz BP
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92.0%;
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BF380737/C
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/dev_grage="Adult"
/clone_lib="UT0073"
/clone_lib="UT0073"
/clone_lib="UT0073"
/clone_logan: uterus_tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-UT00773-170900-167-H01&t2=2000-09-17&t4=1)
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                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 TCTCCTCCCCCCTTCCTTCCCACCCTCAAGTCTGACGATGACACCTCCCAATTTTGATGAA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 6.2e-84;
0; Mismatches 8;
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High quality sequence stop: 339.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapier
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/db_xref="taxon:9606"
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Job time : 4490.47 secs
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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

March 19, 2005, 06:24:41; Search time 749.892 Seconds (without alignments) 11691.196 Million cell updates/sec Run on:

US-10-724-594-1_COPY_17_1497 1481 1 tcaaatatggagcgcggaat......cccggggccgctgctggctc 1481 Perfect

score:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* Database

geneseqn2003cs:*geneseqn2003ds:*geneseqn2004as:*geneseqn2004bs:* genesequ1980s:* genesequ200s:* genesequ200s:* genesequ2001as:* genesequ2001bs:* genesequ2002s:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aca61394 cDNA enco	Aad59938 Human kin	Ado40591 Human kin	Abz68726 Nucleotid	Aad26454 Human kin	Abz68725 Nucleotid	Ada05643 Human NOV	Abq78871 Human kin	Aal55217 Human CRI	Abq78870 Human kin		Aad38864 Human kin	Aal55215 Human CRI	Adn62808 Human NOV	Adf60993 ORF of pa	Aad39191 Human MDP	Adf60992 Pain asso	Adq89099 Hūman uro	Aas06701 Polynucle	Adj96544 Human cit
SUMMARIES	ID	ACA61394	AAD59938	ADO40591	ABZ68726	AAD26454	ABZ68725	ADA05643	ABQ78871	AAL55217	ABQ78870	AAL55214	AAD38864	AAL55215	ADN62808	ADF60993	AAD39191	ADF60992	ADQ89099	AAS06701	ADJ96544
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d	Query Match	100.0	100.0	100.0	99.8	99.7	99.4	93.7	93.7	93.7	93.7	93.7	93.7	93.7	. 93.5	93.3	93.3	93.3	93.3	92.6	95.6
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ALIGNMENTS

Human; ss; gene; gene therapy; kinase; antisense. 1. .6 /*tag= a 7. .1500 /*tag= b /product= "Kinase" 1501. .1515 /*tag= c Location/Qualifiers cDNA encoding novel human kinase. ACA61394 standard; cDNA; 1515 BP. (first entry) Homo sapiens. 11-AUG-2003 ACA61394; Key 5'UTR 3'UTR RESULT 1 ACA61394 CDS

US2003022340-A1

30-JAN-2003.

11-SEP-2002; 2002US-00238709

13-MAR-2001; 2001US-00804471

(APPL-) APPLERA CORP.

Beasley EM; Di Francesco V, Webster M, Yan C,

WPI; 2003-438978/41. P-PSDB; ABU10126.

New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.

780 796 856 900 916 960 1020 1036 1080 1096 1140 1200 1216 1260 1276

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1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTTCGGGTCTGGACTCCCCTGCCAAGA 1320
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                                        The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase.

The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for monitoring the effectiveness of modulating compounds on the expression or ectivity of the transporter gene in clinical trials or in treatment regimen, in gene expression in cells, tissue and organisms. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human kinase proteins and nucleic acids encoding them all of which are useful in the development of human therapeutics and diagnostic composition and methods. The invention is useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic proteins and serve as targets for the drug screening assays, in assays to determine the biological activity of the protein, to raise antibodies and to elicit another immune response. The antibodies are useful in pharamacogenomic analysis, for inhibiting protein function and for tissue typing. The transgenic animals are useful for studying the function of kinase protein, identifying and evaluating modulators of kinase protein activity. The invention is also used in gene therappy. The present sequence 1s the human kinase cDNA. The human, kinase gene is located on chromosome 12
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therapeutic targets, or for treating a disorder associated with an
absence of, inappropriate or unwanted expression of the protein, e.g.
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DI FRANCESCO V
BEASLEY E M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide. The polypeptide and polynucleotide of the invention are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The invention is also useful for biological assays related to kinases. The invention is also useful treating disorders characterized by an absence of inappropriate and unwanted expression of the protein. The present sequence is human kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human kinase proteins and nucleic acids, useful for developing human therapeutic targets, identifying therapeutic proteins serve as targets for the development of human therapeutic agents that modulate kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention provides a kinase polypeptide and its encoding
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kinase related disorder, human, chromosome 12; gene; ss.
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Matches 1481; Conservative 0; Mismatches
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The present sequence encodes a human citron rho/rac-interacting kinase-short kinase polypeptide. The polymucleotide and polypeptide of the invention are useful in preventing, ameliorating, or treating diseases associated with the polypeptide dysfunction. The expression vector or the reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase-short kinase in a disease, such as obesity or chronic obstructive pulmonary disease. These may also be used for treating obesity/ overweight-associated comorpidities, such as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced fertility, and depression
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                                                                                                                                                                                                                         Sequence 1765 BP; 428 A; 430 C; 444 G; 463 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                      Score 1477.8;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 1479; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chronic obstructive pulmonary disease; hypertension; diabetes; coronary artery disease; hyperlipidaemia; stroke; gallbladder disease; gout; osteoarthritis; sleep apnea; cancer; thrombolic disease; polycystic ovarian syndrome; fertility; depression; gene; ss.
                                                                                                                                                                  CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
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               ACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCCGTGCCAGC
                                           ACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCTGGGCAGC
                                                                           TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACAGCAAGG
                                                                                                                                         CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
                                                                                                                                                                                                       CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA
                                                                                                                                                                                                                                                                        Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.
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1. .1494
/*tag= a
/product= "citron rho/rac-interacting kinase-short kinase"
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2001US-0337130P.
2002US-0375015P.
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25-APR-2002;
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Claim 1; Fig 18; 145pp; English

/*tag= a /product= "Human PKIN-7 protein"

WO200196547-A2.

14. .1507

SDS

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TTCCAGATGACCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1030
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New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.

WPI; 2002-090207/12. P-PSDB; AAE16261.

Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT; Bughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

2000US-0212073P. 2000US-0213467P. 2000US-0215651P. 2000US-0216605P. 2000US-0218372P.

2001WO-US019444

14-JUN-2001; 15-JUN-2000; 30-JUN-2000;

20-DEC-2001

13-JUL-2000; 2000US-0218372P 25-AUG-2000; 2000US-0228056P

(INCY-) INCYTE GENOMICS INC

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Human, kinase, PKIN-7; cancer; leukaemia, adenocarcinoma, osteoarthritis, munue disorder; atherosclerosis, Crohn's disease, Hodgkin's disease; Acquired inmune Deficiency Syndrome, AlDS, Addison's disease; anaemia; allergy, asthma, adult respiratory distress syndrome; multiple sclerosis, autoimmune thyroiditis; bronchitis; diabetes mollitus; osteoporosis; Good pasture's syndrome, Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; eardiovascular disease, hypertension; vasculitis; mycocarditis; obesity; congestive heart failure; ischemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy; ss.
                                                                                                                                         AAD26454 standard; cDNA; 2066
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human kinase PKIN-7 cDNA.
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Location/Qualifiers

Homo sapiens

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The invention relates to human kinase PKIN proteins and their corresponding CDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of FKIN and a composition comprising PKIN antegonist is useful for treating a disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The construction of the pkin of 
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0; Mismatches
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Best Local Similarity 99.8%;
Matches 1478; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human citron rho/rac-interacting kinase-short kinase polypeptide and polynucleotide for preventing or treating diseases associated with the polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary disease.
1224 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACAGCAAGG
                                                              CACTGGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
                                                                                                        CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA
                                                                                                                         CACTGGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
                                                                                                                                                                      Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, citron rho/rac-interacting kinase-short kinase, obesity chronic obstructive pulmonary disease; hypertension, diabetes; coronary artery disease; hyperlipidaemia; stroke; gallbladder (gout; osteoarthritis; sleep apnea; cancer; thrombolic disease; polycystic ovarian syndrome; fertility; depression; gene; ss.
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05-OCT-2001; 2001US-0327435P.
09-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
15-OCT-2001; 2001US-0329144P.
17-OCT-2001; 2001US-0339105P.
22-OCT-2001; 2001US-034162P.
24-OCT-2001; 2001US-034162P.
25-OCT-2001; 2001US-034957P.
01-NOV-2001; 2001US-034957P.
                                                                                                                                                            19-APR-2002; 2002US-037381SP.

19-APR-2002; 2002US-037381SP.

19-APR-2002; 2002US-037381SP.

19-APR-2002; 2002US-037384P.

22-APR-2002; 2002US-0374977P.

16-MAY-2002; 2002US-0381037P.

16-MAY-2002; 2002US-0381042P.

16-MAY-2002; 2002US-0381642P.

28-MAY-2002; 2002US-0381642P.

29-MAY-2002; 2002US-0381642P.

29-MAY-2002; 2002US-038166FP.
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01-OCT-2002; 2002US-00262511
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(CURA-) CURAGEN CORP.

Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; JW, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Bisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. P-PSDB; ADA05644.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 20; Page 100; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or presisposition to
a disease associated with altered levels of expression of the above
copypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
cuse in treating a pathology that is related to an aberrant expression or
above; (10) a method for identifying a potential therapeutic agent for
cuse in treating a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
correnting for a modulator of activity or of latency or predisposition to
corrected a pathology associated with the above polypeptide in a
correctivity of the polypeptide described above; (13) method for modulating
corrections of mammal; and (14) a method for producing the above polypeptide in a
correction and a method for producing and above polypeptide in a
correction and and an antidiabetic, anorectic, antibacterial, virucide,
immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
immunication and an appearance of an another producing and antidiabetic, anorectice antibacterial, virucide,

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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly Citron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence encodes a novel human kinase of the invention
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                                                                                     Novel polynuclectide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, in therapy of disorders and diseases e.g. cancer and pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
93.7%; Score 1388.2; DB 6; Length 5877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5877 BP; 1680 A; 1433 C; 1583 G; 1181 T; 0 U; 0 Other;
                                                                                                                                                                               Disclosure; Page 44-45; 50pp; English.
Friddle CJ;
                                   2002-599796/64
Miranda M,
                                                    P-PSDB; ABB81928
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                                   GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG
                                                                                                           CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT
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Citron rho-interacting kinase, gene therapy, mental disorder, cancer;
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               GTGACTGGTGGTGGGCGGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG
                                                                                      CAGAGGGAACCTCTGCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT
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1. .5877
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02-JUL-2001; 2001US-0301841P. 11-DEC-2001; 2001US-0338651P. 25-APR-2002; 2002US-0375014P.

(FARB) BAYER AG

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WPI; 2003-221576/21.

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antigout; osteopathic; antiarthritic; cytostatic; antidepressant; immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic; neuroprotective; antiinflammatory; antidiabetic; analgesic; human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating; obesity; comorbidities; cancer; anorexia; cachexia; bulimia; central nervous system disorder; chronic obstructive pulmonary disease; Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective; Human CRIK related DNA sequence, SEQ ID No 8. BP AAL55217 standard; DNA; 6156 (first entry) diabetes; pain; ds 01-MAY-2003 AAL55217; RESULT 9

Homo sapiens

251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310

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The invention relates to an isolated polymorecture encouring a numban citron rho/rac-interacting kinase polymorphide. The isolated polymorphide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK)

Colympetide and polymucleotide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obseity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, prostate and colon cancer)

CC cancer including endometrial, breast, prostate and colon cancer)

CC cancers, anxiety disorders, Parkinson's disease or Alzheimer's disorders, anxiety disorders, parkinson's disease or Alzheimer's clisorders, anxiety disorders, parkinson's disease or Alzheimer's clisorders and security bulmonary disease, or diabetes. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing.

CT he expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are cuseful in producing and detecting the polymucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This polymucleotide sequence represents a DNA sequence correlating to the human CRIK protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                  New human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or
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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly Citron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence encodes a novel human kinase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in gene
                                                                                                                                                                                                                Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;
Citron rho-interacting kinase; gene therapy; mental disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, in therapy of disorders and diseases e.g. cancer and pharmacogenomic applications.
                                                                                                                                                                                                                                                                                                                                                                                                    replace(6065,G)
/*tag= b
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                          "Single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .6165
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                                                                                                  BP.
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                           AGTGTCACAAGAT 1403
                                                                                                                                                        (first entry)
                                                                                                  ABQ78870 standard; cDNA;
                                                                                                                                                                                    Human kinase cDNA #1.
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P-PSDB; ABB81927.
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93.7%; Score 1388.2; 99.8%; Pred. No. 0; tive 0; Mismatches

Best Local Similarity 99.8 Matches 1390; Conservative

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Query Match

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1 TCADATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGACCCATTGCCAACCGGG

Sequence 6165 BP; 1735 A; 1550 C; 1679 G; 1201 T; 0 U; 0 Other;

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diseases
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                                                                                           TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACAGGAAGG
                                                                                                                                    CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
              ACACCTCCAATTTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCCGTGCCAGC
                                 1151 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human citron rho/rac-interacting kinase (CRIK) polypeptide polynucleotide, useful in preventing, ameliorating or treating associated with human CRIK dysfunction, e.g. obesity, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CRIK encoding DNA sequence, SEQ ID No 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein"
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11-DEC-2001; 2001US-0338651P.
25-APR-2002; 2002US-0375014P.
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                            CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT
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operiteation. The fundant citizen fine facting, finase (CAXIA) polypeptide and polypurclectide are useful in preventing, ameliorating, creating diseases associated with human CRIK dysfunction such as obesity and obsestly-associated comorbidities (e.g. hypertension, coronary artery can obsestly-associated comorbidities (e.g. hypertension, coronary artery cancer including endometrial, breast, prostate and colon cancer; anorbexta, canchexta, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease, or diabetes. The secan also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, disease. The fusion protein is useful in preparing antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polymucleotide and polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polymucleotide and polypeptide and columnant columnary disease. The fusion protein is useful the will be human CRIK polypeptide. This polymucleotide sequence represents a DNA sequence encoding a human CRIK protein of the invention
citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK)
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Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C; Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB; R, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;
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                                           Location/Qualifiers
55. .6219
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Thangavelu K, Khan FA, Ison CH;
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03-NOV-2000; 2000US-0245708P-
09-NOV-2000; 2000US-0247572P-
16-NOV-2000; 2000US-0249565P-
22-NOV-2000; 2000US-0252730P-
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Best Local Similarity 99.8%;
Matches 1390; Conservative
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P-PSDB; AAE24150.
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Homo sapiens
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diseases
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GTCGGGTCTGGACTCCCCTGCCAAGA
                                                                                                                             CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
                                                                                                                                                                             CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA
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11-DEC-2001; 2001US-0338651P.
25-APR-2002; 2002US-0375014P.
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polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polymucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This polymucleotide sequence represents a DNA sequence relating to the human CRIK protein of the invention
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0; Mismatches
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Best Local Similarity 99.8%;
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The invention relates to isolated NOVX polypeptides and polynucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 3; 395pp; English.
15-OCT-2001; 2001US-0329414P.
17-OCT-2001; 2001US-0330142P.
18-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-034362P.
24-OCT-2001; 2001US-034362P.
29-OCT-2001; 2001US-034362P.
29-OCT-2001; 2001US-034362P.
17-APR-2002; 2001US-034362P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
16-MAY-2002; 2002US-0373816P.
16-MAY-2002; 2002US-038103P.
16-MAY-2002; 2002US-038103P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
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28-MAY-2002; 2002US-0381642P.
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PATTURAJAN M.
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MILLET I.
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CATTERTON E.
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                                                                                        GCCAGAAAGAGAGAGACTGAAGGTCTTTGCTGCTGCCATCCTTTCTTCTCTAAAATTG
               GTGACTGGTGGTCGGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG
                                                          CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT
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   CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTTCCAGCGGTTTTTGAAAT
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05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0327917P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
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Dipippo VA;

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polymucleotides may be used to treat disorders associated with decreased copyrucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify mediators in the production of antibodies and in assays to identify may also be used to medulate NOVX polymeptide antibodies, agonists and artagonists may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotide expression and activity of NOVX polypeptides and polymucleotide may be used in this way to prevent, diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotides may be used in this way to prevent, diagnostic agents for detecting the presence of NOVX in search and disorders, anotexia, cancer, cancer-associated achieves and cancers. And the various dysliptideamias, metabolic disturbances associated with obesity, the metabolic syndrome X and the various dysliptideamias, metabolic disturbances associated with chronic diseases and various cancers. They may also be used as antibaterial nover and a manual agents. The present sequence represents DNA encoding a human NOVX protein.

Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;

120 240 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTC 180 203 480 540 323 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360 CTATGAAAGTGAAGAAGAAGGCTTTATTGGCCCCAGGAGCAGGTTTCATTTTTGAGG 420 443 CACITITICAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600 83 Grrdrichchringchdakgrichagerderakgagaaakgcaaccaacarcharg 383 623 TGACTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 24 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA CTATGAAAGTGAAGAAGAAGACTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG TTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAGTATGCCT TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT ö DB 12; Length 1870; Indels ., 2 93.5%; Score 1385; D llarity 99.6%; Pred. No. 0; Conservative 0; Mismatches Query Match Best Local Similarity Matches 1388; Conserv 61 84 121 144 181 241 264 324 384 444 541 564 204 301 361 421 481 504 g ઠે g 셤 ò ò g ò g 5 8 à 셤 à 셤 임 ò ò

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1 (bases 1 to 1515)
Webster,M., Yan,C., Di Francesco,V. and Beasley,E.M.
Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof Patent: US 6479269-A 1 12-NOV-2002, Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Regulation of human citron rho/rac-interacting kinase-short Petent: WO 03004629-A 8 16-JAN-2003;
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Location/Qualifiers
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99.8%; Score 1477.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1479; Conservative 0; Mismatches
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                                     Score 1476.2;
Pred. No. 0;
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                                     99.7%;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                      ACTGGAACATCGTAACTCTCCCCCCCTTCGTTCCCACCCTCAAGTCTGACGATG
                                                                             GCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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	CTGGGAACATTCGTTGGCCGCACAGGACATTCAAGCTGGTGGATTTTGGATCGCCG CTGAGAACATTCTGTTGGCCGCACAGGACACATCAAGCTGGTGGATTTTTGGATCTTGCCG CTGAGAACATTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTTGGATTTTTGCCCG CTGAGAATTGAACATCAACAAGATGGCAAACTCCCGATTGGGACCCCAGATTACA TGCCTCCTGAAGTGCTGACTGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA TGCCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCCCAGGCTTGGCCT TILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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           TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCGGGGACTTGCTGT
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TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT
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Yu,X.S., Miranda,M. and Friddle,C.J.
Human kinases and polynucleotides encoding tent: US 6734009-A 3 11-MAY-2004;
Location/Qualifiers
1.5877
/ organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                              CGTATATGCCAAGGGATCCGCCCGGGGCCCCTGC 1485
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93.7%; Score 1388.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches
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Sequence 3 from patent US 6734009,
AR534559 AR534559.1 GI:53924886
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1331 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTTCTCGGGACA
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Regulation of human citron rho/rac-interacting kinase
Patent: WO 03004523-A B 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
1. .6156
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 0;
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Sequence 8 from Patent WO03004523.
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             Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
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                                                          Yu,X., Miranda,M. and Friddle,C.J.

Human kinases and polynucleotides encoding the same
Patent: WO 02059325-A 3 01-AUG-2002;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
1. :5877
/organism="Homo sapiens"
/mol_type="unaseigned DNA"
/db_xref="taxon:9606"
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Pred. No. 0;
0; Mismatches
               Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
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Best Local Similarity 99.8
Matches 1390; Conservative
 Homo sapiens
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61 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120 	Qy 121 CTCCTCTTTCCGAGAGGGATATTAGATGCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180 Db 131 CTCCTCTTTCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTC 190	Qy 181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240	OY 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300	OY 301 GITGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360	OY 361 CTATGAAAGTGATGAAGAAGAGGTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420 Db 371 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 430	OY 421 AAGAGGGAACATATTATCTCGAAGCACGAGGCCGTGGATCCCCCAATTACAGTATGCCT 480	OY 481 TTCAGGACAAAAATCACCTITATCTGGTCATGAAATATCAGCCTGGAGGGGACTTGCTGT 540	OY 541 CACTITIGAATAGATAIGAGGACCAGTIAGAIGAAAACCIGAIACAGIITITACCIAGCIG 600	Qy 601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 600 bb 611 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670	Oy 661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGÁTCTGCCG 720 Db 671 CTGAGAACATTCTCGTTGACCGCACAGGACATCAAGCTGGTGGATTTTGGATCTGCCG 730	QY 721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCGGATTACA 780 	781 TGGCTCCTGAAGTGCTGTGATGAACGGGGATGGAAAAGCACCTACGGCCTGGACT 840 	841 GTGACTGGTGGTCAGTGGCTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 900	OY 901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960	OY 961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1020	QY 1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1080 DD 1031 GCCAGAAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTCTCTAAAATTG 1090	1081 ACTGGAACAACTTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1140

ACCESSION AX574425 VERSION VERYWORDS VERYORDS COURCE Homo sapiens (human) ORCANISM Homo sapiens ORCANISM Homo sapiens Character, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS TITLE AUTHORS TITLE AUTHORS TITLE AUTHORS TITLE Cocation/Qualifiers Corganism="Homo sapiens" Lexicon Genetics Incorporated (US) Lexicon Genetics Incorporated (US) Lexicon Genetics Incorporated (US) Lexicon Genetics Incorporated (US) Lorganism="Homo sapiens" ADD_XTEE="Laxon:9606" ONERIGIN ONERY MATCH Best Locat Similarity 99.8%; Pred. No. 0; Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0; ACAATANGGAGCGCGAAATCCTTTGGATGCTGCTGCAGCCGGGG 1 TCAAATANGGAGCGCGAAATCCTTTGGATGCTGCTGAACCCATTGCCAGCCGGG 10 11 TCAAATANGGAGCGCGAAATCCTTTGGATGCTGCTGAACCCATTGCCAGCCGGG 10 11 TCAAATANGGAGCGCGAAATCCTTTGGATGCTGCTGAACCCATTGCCAGCCGGG 10 11 TCAAATANTGGAGCGCGAAATCCTTTGGATGCTGCTGAACCCATTGCCAGCCGGG 10 11 TCAAATANTGGAGCGCGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCAGCCGGGG 10 11 TCAAATANTGGAGCGCGAAATCCTTTGGATGCTGCTGCACCCAGCCGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCAGCCGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGAAATCCTTTGGATGCTGCTGCTGCACCCGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGGATGCTGCTGCTGCTGCACCCGGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGCCAAGCCGGGGGG 10 11 TCAAATANTGGAGCGCGGAAATCCTTTGCCAAGCCGCGGGGGGAAATTGCCAAGCCGGGGGGAAATCCTTGCCAAGCCGGGGGGAAATCCTTTGCCAAGCCGGGGGGGAAATCCTTTGCCAAGCCGGGGGGGAAATCCTTTGCCAAGCCGGGGGGGG	Oy 61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120	241 251 301 311 361 371 421	1
421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCT [DD 791 TGGCTCCTGAAGTGCTGACTGTGAAGGGGATGGAAAAGGCACCTACGGCCTGGACT 850	1021 GCCGGAAAGAGAACTGAAGTTTTGAAGGCCTTTGCTGCCTTCTTCTTCTTCTAAATTG 108	QY 1261 CACTGGGGATTCTTGGTAGATCTGTTGTGTCGGACTCCCTGCCAAGA 1320 Db 1271 CACTGGGGATTCTTGGTAGATCTGTTGTTGGACTCCCTGCCAAGA 1330 QY 1321 CTAGCTCCATGGAAAGAAACTTCTCATCAAAGCAAAGAACTTCTCATCAAAGCAAAGAACTTCTCATCAAAGCAAAGAACTTCTCATCAAAAGCAAAGAACTTCTCATCAAAAGAAACTTCTCATCAAAAGCAAAGAACTTCTCATCAAAAGAAACTTCTCATCAAAAGAAACTTCTCATCAAAAGAAACTTCTCATCAAAAGAAACTTCTCATCAAAAGAAACTTCTCATCAAAAGAAACTACAAAAAAAA

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                    TGGCTCCTGAAGTGCTGACTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
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Regulation of human citron rho/rac-interacting kinase Patent: WO 03004523-A 1 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
1. .6165
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/mol_type="unassigned DNA"
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Best Local Similarity 99.8%;
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AGTGTCACAAGAT 1403
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09 1081 ACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACCTCAAGTCCGACGATG 1140 Db 1091 ACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCTCCAAGTCTAACGATG 1150 09 1141 ACACCTCCAATTTGATGAACAGAGAAATTCGTGGGTTTCATCCTCTCTCGTGCAGC 1200 1151 ACACCTCCAATTTTGATGAACAGAGAAATTCGTGGGTTTCATCCTCTCTCGTGCAGC 1200 1201 TGAGCCTCCAAGATTTTGATGAACAGAAAATTCGTGGGTTTTCATCCTCTCTCGTGCAGC 1200 09 1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTACACACAAGG 1200 1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTACACACAAGG 1200 09 1261 CACTGGGGATTCTTGGTAGAACTGACCGTTTGTGTGGGGTTTTCGTACACACAC	1321 CTAGCTCCATGGAAAGAAACTTCTCATCAAAGGAGAGTACCAGGACA	AX504254 AX504254 LOCUS DEFINITION Sequence 43 from Patent W00233099. ACCESSION AX504254 AX504254 AX504254 AX504254 AX504254 AX504254.1 GI:23386094 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) AX504254.1 GI:23386094 KEYWORDS SOURCE Mammalia; Butheria; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	Arvizu, C., Yao, M.G., Rankumar, J., Ding, L., Tang, Y.T., Hafalia, A.J., Nguyen, D.B., Gandhi, A.R., Lu.Y., Vue, H., Burford, N., Bandman, O., Tribouley, C.M., Lal, P.G., Recipon, S.A., Lu, D.A., Borowsky, M.L., Thornton, M., Swarnaker, A., Thangavelu, K., Khan, F.A. and Ison, C.H. JOURNAL Partent: WO 0233099-A 43 25-APR-2002; Incyte Genomics, Inc. (US) FRATURES Location/Qualifiers Source Cocation/Qualifiers	Ouery Match 93.7%; Score 1388.2; DB 6; Length 6298; Best Local Similarity 99.8%; Pred. No. 0; Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 1 TCAAATATGGGGGGGGAATCCTTTGGATGCTGGTGCTGAACCCATTGCGAACCGGG	OY CONCOME CONTROLLED TO THE CONTROLLED CONT

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AY257469 8576 bp mRNA linear PRI 23-APR-2003 Homo sapiens rho/rac-interacting citron kinase (CIT) mRNA, complete
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LALEKEKARCAELEEALQKTRI IELRSAREEAHRKAYDHPHSTPATARQQJAMSA IV
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SHLPAQPDISPNIFEAVKGCHLFGAGKIENGLCICAAMPSKVVILRYNENLSKYCIRK
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RMVTALESVVAGGRVSREKABADAKLLGNSLLKLEGDDRLDMNCTLPFSDQVVLVGTE
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission.
Submitsed (18-MAR-2003) Department of Blochemistry and Molecular
Biology, Baaic Medicine, Suzhou University, Renming Road 48,
Suzhou, Jiangsu 215007, China
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CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960

Db 131 CTCCTCTTTCCCGAGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTCCACACACA	Db 191 AGCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACACAC	251	Oy 301 GTTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAAAGCAACGGGGACTTTTGTG	Qy 361 CTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTCATTTTTGAGG	QY 421 AAGAGGGAACATATTATCTCGAAGCCAAGGCCGTGGATCCCCCAATTACAGTATGCCT	OY 481 TTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT	Oy 541 CACTITIGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTITIACCTAGCTG	Oy 601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC	Oy 661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGATTTTGGATCTGCCG	Oy 721 CGAAAATGAATTCAAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA	Db 791 TGGCTCCTGAAGTGCTGATGAACGGGGATGGAAAAGGCACCTACGCCTGGACT	Qy 841 GTGACTGGTCAGTGGGGGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG Db 851 GTGACTGGTGGTCAGTGGGGGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG	Oy GGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGGGTTTTTGAAAT 	Qy 961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGGGGGGGG	Qy 1021 GCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCTGCCTTTCTTCTTCTAAAATTG	Oy 1081 ACTGGAACAACTTCGTACTCTCCCCCCTTCGTTCCCCCCTCAAGTCCGACGATG	Qy	Qy
Db 964 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGGGTTTTTGAAAT 1023 Ov 961 TTCCAGATGACCCCAAAGTGACTATCTTGAATTTCCAAAGTTGTGTGT	1024 TICCAGAIGACCCCAAAGIGAGCAGIGACTITCIIGATCIGATICAAAGCTIGIIGCG	Qy 1021 GCCAGAAAGAGAGTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTCTAAAATTG 1080	Qy 1081 ACTGGAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCTCAAGTCCGACGATG 1140 Db 1144 ACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCTCAAGTCTGACGATG 1203	CCAGC		CACTGGGGATTCTTGGTAGATCTGGTGTGTGGGGTCTGGACTCCCCTGCCAAGA 132	1321 CTAGCTCCATGGAAAGAAACTTCTCATCAAAGGAAGGGCTACAGAGCTTCTCAGGACA 138	1381 AGTGTCACAAGGT 1393 	SULT 14	AASTIUS AX671108 8603 bp DNA linear PAT 27-MAR-2003 DEFINITION Sequence 4 from Patent WO03004523. ACCESION AX671108 AX67	S Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 AUTHORS Zhu,Z.	Regulation or Patent: WO 0 Bayer Aktien	SOURCE 1	Query Match Query Local Similarity 93.7%; Score 1388.2; DB 6; Length 8603; Best Local Similarity 99.8%; Pred. No. 0; Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	GAGGGGGAATCCTTTGGATGCTGGTGCTGGTGACCCATTGCCAACGGG 60	CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT	121 CTCCTCTTCCCGAGAAGGATATTAGATGCCCTCTTTGTTCTTTGAAGAATGCAGTC 18

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964 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 1023
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                                                                                                                                                     GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG
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                      244 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA
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                                                                                                                                      GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG
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/protein id="AAP43922.1"
/db xref="citron"
/db xref="citron"
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HRDIKPENILVDRTGHIKLVDFGSAAKMISNKMYNAKLPIGTPDYMAPEVLTVMNGDG
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LLIKSKELQDSQDKCHKMEQEMTRLHRRVSGG"
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

Mao, Y., Xie, Y. and Wu, Q.

Cloning and characterizing a novel human CRIK-SK gene
Unpublished

2 (bases 1 to 1799)

Mao, Y., Xie, Y. and Wu, Q.

Direct Submission

Submitted (02-JAN-2003) Institute of Genetics, Fudan University,
220 Handan Road, Shanghai 200433, P.R. China

Location/Qualifiers
                                                                                 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAAGATCTCTCAGGACA
                                                                CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA
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/organism="Homo sapiens"
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-311-034-33
US-10-262-511-3
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231.4 15.3 228 15.0 228 15.0 225.6 14.9	44.0	157-1 130-9 130-1	equence 179, equence 99, equence 101, quence 1, Ap

ALIGNMENTS

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Sequence 1, Application US/09804471A

Sequence 1, Application US/09804471A

Patent No. US20020132322A1

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REPERENCE: CL001164

CURRENT APPLICATION NUMBER: US/09/804,471A

CURRENT FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 4

SEQ ID NOS: 4

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Best Local Similarity 100.
Matches 1515, Conservative
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ORGANISM: Human
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Sequence 1, Application US/10724594

Publication No. US20040091993A1

GENERAL INFORMATION:

APPLICANT: WEBSTER, Marion et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOFF

TITLE OF INVENTION: AND USES

TITLE OF IN
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100.0%; Score 1515;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches
GCCGCCTGATCCGTA 1515
                    ; ORGANISM: Homo sapiens
US-10-724-594-1
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TRIBOULEY, Catherine M. CHAWLA, Narinder K. YAO, Monique G. LU, Dyung Aina M. LU, Dyung Aina M.
                                                                                                                                                                                       HAFALIA, April
ARVIZU, Chandra S.
GURURAJAN, Rajagopal
                                                          GREENWALD, Sara R. RAMKUMAR, Jayalaxmi GRIFFIN, Jennifer A.
                                                                                                                                                                                                                                                                            POLICKY, Jennifer L.
                                                                                                            BURFORD, Neil
NGUYEN, Danniel B.
TANG, Y. Tom
BAUGHN, Mariah R.
                                                                                                                                                                                                                                       KHAH, Farrah A.
RECIPON, Shirley A.
AZIMZAI, Yalda
                                                                                                                                                               HE, Ann
THORNTON, Michael
                                                                                                                                                                                                                                                                                        DING, Li
GRETHER, Megan
                                                                                                   KEARNEY, Liam
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              GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT
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APPLICANT: ELLIOTT, VICKI S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: BATRA, Sajeev
APPLICANT: BATRA, Sajeev
APPLICANT: BATRA, Sajeev
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; 60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-06.
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; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CB1
US-10-311-034-33
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Best Local Similarity 99.8
Matches 1512; Conservative
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SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 2066
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US-10-311-034-33
; Sequence 33, Application US/10311034
; Sequence 33, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BANDMAN, Olga
; APPLICANT: AU-YOUNG, Janice
, APPLICANT: LU, Yan

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APPLICANT: Agee, Michele L.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: 04/226,483
PRIOR PILING DATE: 2003-05-28
PRIOR PILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
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US-10-262-511-3
Sequence 3, Application US/10262511
Sequence 3, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Seyman, John A.
APPLICANT: Rekuda, Ramesh
APPLICANT: Li, Li, Li, Li, APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
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Stone, David J.
Pena, Carol B. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark B.
Leach, Martin D.
Agee, Michele L.
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Malyankar, Uriel M.
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Ji, Welzhen
Miller, Charles E.
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Anderson, David W.
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                                                                         3; Indels
                                 92.7%; Score 1404.2;
llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
                                   Query Match
Best Local Similarity
Matches 1406; Conserv
JS-10-415-011-43
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RESULT 7
US-10-028-946-3
US-10-028-946-3
Sequence 3, Application US/10028946
Fublication No. US20020123622A1
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchunian
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: NO. US20020123622A1e1 Human Kinases and Polynucleotides Encoding t
TITLE OF INVENTION: NO. US20020123622A1e1 Human Kinases and Polynucleotides Encoding t
CURRENT FILING DATE: 2001-12-20
FRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5877
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       614 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCATGGGATACGTGCATCGA
                                                               674 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT
                                                                                                                  GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR PILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-04-17
PRIOR PRIOR PRIOR DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2001-10-05
PRIOR PILING DATE: 2001-10-05
PRIOR PILING DATE: 2001-10-05
PRIOR PRIOR PILICATION NUMBER: 60/373,435
PRIOR PILING DATE: 2001-10-05
PRIOR PRIOR PILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: CDS
; LOCATION: (2)..(1870)
US-10-262-511-3
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1870
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	Qy 1147 TCCGACGATGACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCATCTCT 1206	1201 CCGTGCCAGCTGAGCCCTTCTCGGTGAAGAACTGCCGTTTGTGGGGTTTTTCG 1267 MACAGCCAAGCTGAGGCTTCTCGGGTGAAGAACTGCCGTTTTTGTGGGGTTTTTTCG 1267 MACAGCAAGCTGAAGTGTTTTTTCGTGGGGTTTTTTCGTGGGGTTTTTTCGTGGGGTTTTTT	TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTTGTGTGGGGTCTGGACTCCCCCAAGGCACTCTGGAGTTCTGGACTCCCCCAAGGCAAGGCAAAGGAAAAAAAA	1321 CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGAC 138	TCTCAGGACAAGTGTCACAAGAT	RESULT 8 US-10-791-666-3 ; Sequence 3, Application US/10791666	GENERAL INFORMATION GENERAL INFORMATION APPLICANT: Yu, Xuanchuan APPLICANT: Miranda, Maricar APPLICANT: Miranda,	; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same; FILE REFERENCE: LEX-0289-USA; CURRENT APPLICATION NUMBER: US/10/791,666	FRIOR APPLICATION NUMBER: US10/028,946 PRIOR FILING DATE: 2001-12-20 PRIOR PILING DATE: 2001-12-20 PRIOR PART OF APPLICATION NUMBER: US 60/258,335	NUMBER OF SEC ID NOS: 4 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 3 ; TENUME.	Ω	Query Match 92.3%; Score 1398.2; DB 18; Length 5877; Best Local Similarity 99.8%; Pred. No. 0; Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Oy 7 AIGITGAAGITCAAATAIGGAGCGCGGAAICCITIGGAIGCTGGTGCTGACCGAIT 66	Qy 67 GCCAACGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATGACTCAA 126	Qy 127 CAGCAGATGTCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186	Qy 187 GAATGCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
TYPE: DNA ORGANISM: homo sapiens Core 1398.2; DB 13; Length 5877; Ouery Match 92.3%; Score 1398.2; DB 13; Length 5877; Ouery Match 99.8%; Pred. No. 0; Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Mismatches Ouery Matches 1400; Conservative Ouery Matches O	Qy 67 GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAA 126	Oy 127 CAGCAGAIGICTCCTCTTTCCCGAGAAGGGAIATTAGATGCCCTCTTTGTAT 186	Oy 187 GAATGCAGTCAGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 246	OY 247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA 306	OY 307 AGTCTIGTAGGTIGGGCCACTTTGCTGAAGTGCAGGTGGTAGAGAGAAAGCAACCGGG 366	Oy 367 GACATCTATGCTATGAAGAGAGAGAGAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 426	OY 427 ITITICAGGAAGAGGGAACATAITAICICGAAGCACAGAGCCCGGGATCCCCCAAITA 486	OY 487 CAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 546	Oy 547 GACTTGCTGTCACTTTCAATAGATATGAGACCAGTTAGATGAAACCTGATACAGTTT 606	Oy 607 TACCTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 666	Oy 667 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGATTT 726 	OY 727 GGATCTGCCGCGAAAATGAATTCAAACAAGGTGAATGCCAAACTCCCGATTGGGACC 786 	OY 787 CCAGATTACATGGCTCCTGAAGTGCTGACTGATGAACGGGGATGGAAAAGGCACCTAC 846	Qy 847 GGCCTGGACTGGGGGGGGGGGGTGGATTGCCTATGAGATGATTTATGGGAGA 906 Db 841 GGCCTGGACTGTGACTGGTGGTCAGTGGGGCGTGATTGCCTATGAGATGATTATGGGAGA 900	OY 907 TCCCCTTCGCAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966	967 ITTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026

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APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. 0220020123622Alel Human Kinases and Polymucleotides Encoding
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US 60/258,335
PRIOR FILING DATE: 2000-12-7
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6165
                            1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTGTCGGGTCTGGACTCC 1320
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Pred. No. 0;
0; Mismatches
                                                                                 1387 TCTCAGGACAAGTGTCACAAGGT 1409
                                                                                                1381 TCTCAGGACAAGTGTCACAAGAT 1403
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Best Local Similarity 99.8%;
Matches 1400; Conservative
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Pred. No. 0;
0; Mismatches
PRIOR APPLICATION NUMBER: US/10/028,946
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-12-20
PRIOR PILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6165
TYPE: DNA
ORGANISM: homo sapiens
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Best Local Similarity 99.8%;
Matches 1400; Conservative
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Publication No. US20040209297A1
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/791,666
CURRENT FILING DATE: 2004-03-02
                                                                      GACATCAAGCCTGAGAAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT
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### APPLICANT: Stoles Santisgo, Immaculada
### APPLICANT: Stoles Santisg
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Pred. No. 0;
0; Mismatches
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92.3%;
Best Local Similarity 99.5%;
Matches 1402; Conservative 0
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Sequence 11, Application US/10325430

Publication No. US20030153525A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Rosenfeld, Unie Beth

TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING

TITLE OF INVENTION: A2238, 336 and 52908

TITLE OF INVENTION: 3238, 336 and 52908

TITLE OF INVENTION: 32038, 336 and 52908

TITLE OF INVENTION: 32038, 336 and 52908

TITLE OF INVENTION: WIMBER: US 60/341,953

PRIOR FILING DATE: 2002-12-19

WIMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 4.0

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                                                                              Sequence 3, Application US/10017216

Publication No. US20020160483A1

GENERAL INFORMATION

APPLICANT: KAPELLER-LIBERMANN, Rosana

TITLE OF INVENTION: 13345, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prof

TITLE OF INVENTION: Kinase and Uses Therefor

TITLE OF INVENTION: Kinase and Uses Therefor

FILE REFERENCE: 10147-57U1

CURRENT APPLICATION NUMBER: US/10/017,216

CURRENT APPLICATION NUMBER: US 60/242,429

PRIOR FILING DATE: 2000-10-23

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
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                                    Score 1391.8;
Pred. No. 0;
0; Mismatches
                                    Query Match
Best Local Similarity 99.5%;
Matches 1396; Conservative
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
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CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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Best Local Similarity 99.8%;
Matches 1400; Conservative 0
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APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides |
PILE REPERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
               Sequence 3, Application US/10028946
Patent No. 6734009
GENERAL INFORMATION:
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Sequence 1, Application US/09916204
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Sequence 1, Application US/09916204
GRNERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE OF INVENTION: THEREOF
FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERBYCE: CLOO1164CIP
CURRENT APPLICATION NUMBER: US/09/916,204
CURRENT FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FasteseQ for Windows Version 4.0
SEQ ID NO:
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ORGANISM: Human
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US-09-774-528-419
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-774-528-419
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Sequence 1, Application US/10282048

Patent No. 6692948

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al.

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

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                                                                                                                                   CCCATTGCCAGCCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATG 167
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TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOJ307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PLILIG DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
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Score 760.8; DB 4;
Pred. No. 5.3e-244;
0; Mismatches 2;
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; Sequence 2640, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:
Query Match 50.2%;
Best Local Similarity 99.7%;
Matches 762; Conservative
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                    1858 IGTCTGAAAATGCTAAAGGATCTTATTCGAAGGCTCATTTGTAGCAGAGAACATCGACTTG 1917
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APPLICANT: Brook, J. David
APPLICANT: Houseman, David E.
APPLICANT: Harley, Helen G.
APPLICANT: Johnson, Keith J.
APPLICANT: Johnson, Keith J.
APPLICANT: JOHNSON: RENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Militia Drive
STREET: Two Militia Drive
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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELEFRONE: 617-861-6240
TELEFRAX: 617-861-6240
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FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
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APPLICATION NUMBER: US/08/422,699A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/422,706
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CITY: Lexington
STATE: Massachu
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US-08-422-699A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 GCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGA 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 TGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGCGCG 877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938 CCTTCAATAACAITATGAATTTCCAGCGGTTTTTGAAATTTCCAG---ATGACCCCCAAAG 994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 ATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGTCACTTTTGAATAGATATGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 GAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCTTTCAGGACAAAATCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCC
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                                                                                                                                                                                                                                                                                                                      Score 234.6; DB 4; Length 2423;
Pred. No. 2.9e-67;
0; Mismatches 519; Indels 15;
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2640
LENGTH: 2423
                                                                                                                                                                                                                                                                                                                         15.5%;
                                                                                                                                                                                                                                                                                                                                                                             Matches 591; Conservative
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                  US-09-949-016-2640
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Length 2726;
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                                                                                                                                                                                                                                                                       APPLICANT: Brook, J. David
APPLICANT: Brook, J. David B.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                         DNA SEQUENCE ENCODING THE MYOTONIC DYSTROPHY GENE AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 225:6; DB 2;
Pred. No. 3.3e-64;
0; Mismatches 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.30
                                                                     1145 AGTCCGACGATGACACCTCCAATTTTGA 1172
                                                                                                             1203 Aaggreccacceacacarecaacricea 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEPAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                    Sequence 12, Application US/08422706B Patent No. 5977333 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%;
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Best Local Similarity
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                                                                                                                                                                                                         JS-08-422-706B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cececgagarecrigeaggererideggeggreggererigggenenggererigggegererigg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGCCTG 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCGCGA 739
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                                                                                                                                                                                                                                                                                                                243 cceaacricecccaecacaacaacracerececeacrirerrecaerececeaececarceres 302
                                                                                                                                                                                                                                                                                                                                                          260 CTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTT 319
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                                                                                                                                                                                                                                                                       CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACATAG
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                                                                                                                                                                                                                             15;
                                                                                                                                                                                     Length 2726;
                                                                                                                                                                                Score 225.6; DB 2; Length
Pred. No. 3.3e-64;
0; Mismatches 439; Indels
                                                                                                                                                                                     Query Match
Best Local Similarity 54.0%;
Matches 534; Conservative
                                                   LENGTH: 2726 base pairs;
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
;
TOPOLOGY: linear
US-08-422-699A-12
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1034
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APPLICANT: Brook, J. David
APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNS SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DNSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 218.8; DB 2;
Pred. No. 6e-62;
0; Mismatches 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                         E: Hamilton, Brook, Smith & Reynolds,
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-192
ATTORNEY/AGENT INFORMATION:
NAME: GTANAHAN, PARTICIA
REGISTRATION NUMBER: 32.227
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
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APPLICATION NUMBER: US/08/422,699A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.5%;
Matches 511; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2511 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
. US
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Mil:
CITY: Lexington
STATE: Massachus
Patent No. 5955265
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; LOCATION:
US-08-422-699A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGTCAC 559
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                                    CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAG 259
                                                                                                         243 CCGAACTGGCCCAGGACAAGTACGTGGCCGACTTCTTGCAGTGGGCCGAGCCCATCGTGG 302
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310 CTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGAC 369 250 GACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGT 309 43 eccarceregregaegerraagaagsreegaereegaegaegaegaerreegaeg 102 15; Gaps Length 2511; Indels

> ; Sequence 8, Application US/08422699A RESULT 11 US-08-422-699A-8

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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/422,706B FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOWUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
APPLICATION NUMBER: US 08/284,543
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                                                                                                                                                                            COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 54.5%;
Matches 511; Conservative
                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2511 base pairs
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LENGTH: 2511 base pair
                                                                     Massachusetts
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                     COMPUTER READABLE FORM:
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US-08-422-706B-8
                                                                                         COUNTRY:
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                                                                                                                                                                 GATTACATGGCTCCTGA---AGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTAC 846
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    103 GTGATCGGACGCGGGGCGTTCAGCGAGGTAGCGGTAGTGAAGATGAAGCAGACGGCCCAG 162
                                                370 ATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTT 429
                                                                                         163 GTGTATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGAGGTGTCGTGC 222
                                                                                                                                     430 TTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAG 489
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250 GACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGGTCAGAAGT 309
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     Length 2511;
                                                 Indels
Score 218.8; DB 2;
Pred. No. 6e-62;
0; Mismatches 412;
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Sequence 8, Application US/08422706B

Patent No. 597333

GENERAL INFORMATION:

APPLICANT: Brook, J. David

APPLICANT: Housman, David B.

APPLICANT: Harley, Helen G.

APPLICANT: Harley, Helen G.

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC

TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

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983 cecerrecaesareaeaacracereraceresecareareaararracereseceseseaeer 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 14.4%; Score 218.4; DB 1; Local Similarity 54.5%; Pred. No. 9.6e-62; les 510; Conservative 0; Mismatches 411;
                                                                                     US 08/019,940
      APPLICATION NUMBER: US/08/484,044
                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: PAUL, THOMBER: 32,714
REFERENCE/DOCKET NUMBER: D-54.
TELECPHONE: 713/651-525
TELEPHONE: 713/651-525
                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                    3182 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-484-044-11
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TTCGCCTTCCAGGATGAGAACTACCTGGTCATGGAGTATTACGTGGGGGGGAC 342
                                                                                       CHGCTGACACTGCTGAGGTTTGGGGAGCGATTCCGGCCGAGATGGCGCGCTTCTAC 402
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Patent No. 5552282

GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Fi, Wing-Hui
APPLICANT: Friedman, David L.
APPLICANT: Friedman, David L.
APPLICANT: Friedman, David L.
APPLICANT: Fenwick, Raymond G.
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCACCCTCAAGTCCGACGATGACACCTCCAATTTTGA 1172
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ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Fulbright & Jaworski, L.L.P
1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Houston
STATE: Texas
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US-08-484-044-11
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APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION:
TITLE OF INVENTION:
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOI164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT PILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174493
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Fatent No. 6680188
FATENT NO. 6680188
FATENT NO. 6680188
FATENT NO. FATENT
                                                                                                                                                                                                                                                                                                                                                                                                                               1077 TCCTTTCTTCTTCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCC 1136
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                                                                                 969 TTTGAAATTTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCTGATTCAAAG 1025
                                                                                                                                                                       1026 CTTGTTGTGCGCCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC------CA 1076
                                                                                                                                                                                                                                                                                                                                              1523 GTTGCTGTGTCCCCCCGGAGACACGGCTGGGCCCGGGGTGGAGCAGGCGACTTCCGGACACA 1582
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1403 GCCCTTCTACGCGGATTCCACGGCGGAGACCTATGGCAAGATCGTCCACTACAAGGAGCA 1462
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14.3%; Score 216.2; DB 4; Length 174493;
Best Local Similarity 96.5%; Pred. No. 8.7e-60;
Matches 221; Conservative 0; Mismatches 8; Indels 0;
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; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3
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ORGANISM: Human
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Pred. No. 8.7e-60;
0; Mismatches 8;
FILE REFERENCE: CL001164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PREISEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174493
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time: 271.502 secs
                                                                                                                                                                                              NAME/KEY: misc_feature
| LOCATION: (1)...(174493)
| OTHER INFORMATION: n = A.T.C or
US-10-238-709-3
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Best Local Similarity 96.5
Matches 221; Conservative
                                                                                                                                       TYPE: DNA
ORGANISM: Human
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BM904785 AGENCOURT
CR746615 CR746615
BG808196 2082-86 M
CR746792 CR746792
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OST45250
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                                                                                                                                                                                                                                                                1. ggggagatgttgaagttcaa......tctgagccgcctgatccgta 1515
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BC008127
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum DB seq length: 200000000
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9b_htc:

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Perfect score:
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100110	10011	238.8 15.8 237.2 15.7 233.6 15.4 233.4 15.4 231.4 15.3 225.2 14.9	BP146990 BP14690 BP146990 BP14690 BP1469	~ 0
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∠ 000401	- L R R L A		general party of the control of the	ip=,
CK841805 BB827314 BR018641 CG655761 BF944809 CB783081	CF/445826 CF744580 BU475240 BU467302 CK147448 BY602044	BC024150 BC026615 BC026615 BP168081 CD310916 BY021399 BC038993 AL360718	ALICHMENTS 698 bp mRR riched swine cl 0025B09 5', mRR anticodactyla; 8 Suzuki,K., Sawe anticodactyla; 8 constructor of the constructor of clones derived the constructor of clon	full-length enriched
CK841805 BB827314 BY018641 CG655761 BF944809	CF744826 CF744580 BU475240 BU467302 CK147448 BY602044	BC024150 BC05615 AY408615 AY40801 BP168081 CD310916 BY021399 BB823725 BC038993 AL360718	ry, ad ce. ad ce. data; idae; Toki, Toki, onal I oligo-	swine cDNA li
UI-R-BJ0p BB827314 BY018641 OST426725 PM3-NN117 AMGNNUC:N		Mus muscu S Mus muscu 1 Bpl6881 6 StrPu691. 9 BY02139 5 BB823725 3 Homo sapi		brary, adult

Length 698;

39.8%; Score 602.6; DB 5; 91.4%; Pred. No. 2.9e-172;

Query Match Best Local Similarity

ORIGIN

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Matches

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/lab_host="bl108"
/clone lib="NHI MGC 72"
/note="Organ: 8kin; Vector: pGMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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_6699306 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557590
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1085)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                    AATATGATACAGTTTTTACCTAGCTGAAATGATTTTGGCTGTTCACAGCGTTCATCAGATG
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                                                       CAGGAGCAGGTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Praction: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
            ö
            60; Indels
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BM904785.1 GI:19355164
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          638; Conservative
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BG808196
2082-86 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA,
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                                                                                                                                                                                                                                            Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 600)
Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
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Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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86.6%; Pred. No. 1.9e-126;
ive 0; Mismatches 77;
                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                       BG808196.1 GI:17955172
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Best Local Similarity 86.6
Matches 499; Conservative
      485 CATGGAAA 492
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                                                                                               Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAG998D0712279.
RZPDILB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 110
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 TGACCCCCAAAGTGAGGGAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCGGCCAGAA 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924 AACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAATTTCCAGA 983
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1 (bases 1 to 492)
Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., I
Betrs, M., Radelof, U. and Schneider, D.
I.M. A.G.E. cDNA Clone Collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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Matches 481; Conservative
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BG944539 427 bp mRNA linear EST 15-JAN-2003 ax51f11.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library) Homo sapiens cDNA clone ax51f11 random, mRNA sequence.
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                                                                                                                   300
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1 (bases I to 427)

Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.

Gene expression in proliferating human erythroid cells

Genomics 59 (2), 168-177 (1999)
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Laboratory of Chemical Biology
Mational Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda,
20892, USA
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library)"
                                                 239 TTTGAAGAATGCAGTCAGCCTGCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG
                                                                                                                                                                                                                                                          Grcagaagrcrrgraggrrgrggrcacrrrgcrgaagrgcaggrggraagagaaagca
                                                                                                                                                                                                                                                                                                            361 ACCGGGGACATCTATGCTATGAAAGTGAAGAAGAAGAAGAAGGCTTTATTGGCCCCAGGAGCAG
                                                                                                                                                                                                                                                                                                                                    DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).

Plate: 51 row: f column: 11
Seq primer: -21M13 forward primer (ABI).
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/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="ax51f11"
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EST.
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Fax: 301 435 5148
Email: jm7f@nih.gov
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CR746792 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGp998E239412 ;
IMAGE:4149886 5', mRNA sequence.
                                              540
                                                                         GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGTGAA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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445 GTTTCATTTTTCGAGGAGGAGGAACATATTATCTCGGAGCACGAGTCCTTGGATCCCC 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free from RZPD; contact RXPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mcm."
/mol_type="mcm."
/mol_type="mcm."
/dob_xref="taxon.9606"
/clone="IMAG998B239412; IMAGB.4149886"
/clone=type="glioblastoma with EGFR amplification"
/lab_host="JH10B (T1 phage-resistant)"
/clone=lib="NCI_CGAP_Brn64"
/note="Grgan: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
                                            481 CAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT
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RazD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

Email: www.rzpd.de

Rzpb; IS, I.M.A.G. B. CDNA Clone Collection;

Contact: Inge Arlart

RzpD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100
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                                                                                                                                         541 GGAGGGACTTGCTGTCACTTTGAATAGATATGAG 576
                                                                                                                                                                       GGAGGGGATTTGCTGTCGCTTCTGAACAGATACGAG 600
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www.rzpd.de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGTCACTTTTGAAT 420
                Clontech's Capfinder CDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and clond into EcoRi digested Lambda Zap II vector to in vivo excision in SOLR cells. Individual colonies were grown, and the CDNA inserts were sequenced in high throughput (NIH intramural sequencing center the CDNA inserts were sequenced in high thtp://www.nisc.nih.gov/)."
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Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ik51b06.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to
TR:088937 088937 RHO/RAC-INTERACTING CITRON KINASE SHORT ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus I. (bases 1 to 617)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                            CGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTCAGCCTGCTCTG
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Endocrine Pancreas Consortium
ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Ki
                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                  Length 427;
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                                                                                                                                                                                                                                             Score 423.8; DB 4;
Pred. No. 1.2e-117;
0; Mismatches 2;
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                                                                                                                                                                                                                                                Query Match 28.0%;
Best Local Similarity 99.5%;
Matches 425; Conservative
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                                                                                                                                                                                                   DRIGIN
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/mod_type="mRNA"
/#not_type="mRNA"
/#strain="129/Sv x CD1"
/#db_xerfe="txon:10090"
/#dw stage="p.c. 14.5"
//lab_host="E. coli-DH12S (GIBCO)"
//clone llb="Kaestner ngn3 wt"
//note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_l:
/note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_l:
/not I; Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-SalI sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/-. The wt library is in
pSPORT1, T7 promoter is 5'."
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                                                                                                           Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Scearce
(mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 TTTGAAGAGTGCAGCCAACCCGCCTGATGAAGATGAAGCACGTGAGCAGCTTTGTCCAG 326
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, As 0218
As 0218
Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAAGATGTTGAAGTTCAAGTATGGTGTGCGGGAACCCGCCGGAGGCCAGTGCCTCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                     1. .617
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

RESULT 8 CN682405 LOCUS

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25.1%;
                                                         Matches 426; Conservative
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                                            Similarity
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                              Query Match
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Butaryota; Metazoa; Chordata; Sciurognath; Muridae; Murinae; Mus;

1 (Joases I to 481)

Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B.; Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
Wang,Y., Carter,M.G., Hamatani,T., Alba,R., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,M.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
Transcriptome analysis of mouse stem cells and early embryos

Laboratory of Genetics
            CN682405
481 bp mRNA linear EST 17-MAY-2004
GEO164804-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low
density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04
IMAGE:30782511 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                              National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0164 row: B column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |mol_type="mRNA"
|strain="129Sv|SvTmc"
|db_xref="niaET:E0164B04-5"
|db_xref="taxon:10090"
|clone="NIA:E0164B04 IMAGE:30782511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .481
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                     Mus musculus (house mouse)
                                                                       CN682405
CN682405.1 GI:47448856
                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Reverse
                                                                                                                                   Mus musculus
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source

FEATURES

COMMENT

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CN678533
479 bp mRNA linear EST 17-MAY-2004
E0112C12-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low
density) cDNA library (Long) Mus musculus cDNA clone NIA:E0112C12
IMAGE:30777539 5', mRNA sequence.
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D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.
Plos Biol. 1 (3), 410-419 (2003)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 479)
                                                                                                                                                                                                                                                                                                                                                                                                                                        477 CCCCCAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCA
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
average insert size is about 2.8 kb. The library constructed by Yulan Piao."
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m
                                                                                                                                   Length 481;
                                                                                                                                                                                                 Indels
                                                                                                                               Score 380; DB 7; L
Pred. No. 3.2e-104;
0; Mismatches 55;
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University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1797673
Seq primer: Mil Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 12-DEC-2000
     420
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UI-R-BJOp-aip-b-06-0-UI.rl UI-R-BJOp Rattus norvegicus CDNA clone
UI-R-BJOp-aip-b-06-0-UI 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Normalization and subtraction: two approaches to facilitate gene
                                                                                                                     657 CGTGCATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACACATCAAGCT
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Coordinated Laboratory for Computational Genomics
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                                                                                                                                                                                                                                                                              /db_xref="niaEST:E0112C12-5"
/db_xref="taxon:10090"
/clone="NIA:E0112C12 IMAGE:30777539"
                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="Embryonic Stem Cell"
/cell line="129.3 ES cells"
/lab_host="DH108"
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0112 row: C column: 12
Seg primer: M13 Reverse
High quality sequence stop: 479
POLYA=No.
                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="129Sv/EvTac"
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.0°
Matches 424; Conservative
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Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                22.7%;
nilarity 84.5%;
Conservative 0
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Best Local Simil
Matches 469; (
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                            TTGGAAGAGTGCAGTCAGCCTGCCCTCATGAAGATAAAGCACGTGAGCAGCTTCGTCCGG
                                                                                                                         154 ACTCAACAGCAGATGTCTGCTTTTCCCGGGAAGGGGTGTTAGATGCCCTCTTTGTTCTC
                                                                                                                                                                                                                                                                                                       GGAGAGATGTTGAAGTTCAAGTATGGAGTGCGGAACCCGTCCGAGGCCAGTGCCCCCGAG
                                                                                                        CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATG
                                                                                                                                                                 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC
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                                             GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution information of
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1786 row: 1 column: 17
High quality sequence stop: 648.
Location/Qualifiers
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 Pred. No. 1.8e-95;
0; Mismatches 66; Indels
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="MNRI"
/db_xref="taxon:10090"
/clonne="IMARISE:310496"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTCATTTTTGAGGAAGAGGGGAACATATTATCTC 457
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al Similarity 85.6
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/clone_lib="NCI_CGAP_Mam4" // hote="Organ: mammary; vector: pCMV-SPORT6; Site_l: Sall; Site_l: Shoti; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIM Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
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Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Hangy, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 CCCATTGCCAGTCGGGCCTCCAGGCTAAATCTCTTCTTCCAGGGGAAACCGCCCCTCATG
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Pred. No. 3.5e-93;
0; Mismatches 78;
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CG501399 449 bp mRNA linear GSS 01-0CT-2003 OST45249 Mus musculus cDNA clone OST45249, mRNA sequence. CG501399.1 GI:37275067 GSS01399.1 GI:37275067
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Lo (Asses 1 to 449)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="glioblastoma with EGFR amplification" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NCI CGAP_Brn64" /note="Cogan: brain; vector: pCWV-SPORT6; Site_1: NotI; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average innert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP_Library."
                      Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM9412 row: e column: 23

High quality sequence stop: 423.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 CCGGAAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 CCGGAAGTATTCCGACACCATACTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 423;
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                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4149886"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1244 AACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGT 1303
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Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Yah,Q., Person,C. and Sands,A.T.
Whyl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 423)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1124 CCCCCTTCGTTCCCACCCTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                   Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 450;
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                                                                                                                                                                                                                                                                                                                                                                    | 1.450
| Organism="Mus musculus"
| Mool type="mRNN"
| Atrain="1295V/Bv"
| Ab xref="taxon:10090"
| Colne="Correst AtsSto"
| Cell type="embryonic stem cell"
| Clone_lib="Mus musculus 1295V/Bv"
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Pred. No. 1.1e-88;
0; Mismatches 39;
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Best Local Similarity 90.0%;
Matches 352; Conservative
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LOCUS

RESULT 13

BF344814

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE

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Best Local Similarity 92.0
Matches 346; Conservative
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CG652891.1 GI:37476740
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Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Yeryl, B. W., Ja.-O., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Xu, N., Shu, Q., Person, C. and Sands, A.T. Whil kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                      Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 327; DB 9; Length 449;
Pred. No. 5.1e-88;
0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="embryonic stem cell"
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                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="0ST45249"
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Best Local Similarity 91.8%;
Matches 345; Conservative
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                                                                                                                                                                                                                                                                                                                                                                4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.

Location/Qualifiers
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Zambrowicz B.P., T. Abuin, A., Ramirez-Solis, R., Richter, L.J., Pinch, R.A., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaling, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma. Z.-Q., Markeslch, D., Pane, R., Potter, D.G., Olan, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparke, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T. Whkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.0%; Score 318.2; DB 9; 92.0%; Pred. No. 2.6e-85;
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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GenCore version 5.1.6
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March 19, 2005, 06:24:41; Search time 767.108 Seconds (without alignments) 11691.196 Million cell updates/sec Run on:

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Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn1980s:* geneseqn2000s:* geneseqn2001s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2001bs:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* N_Geneseq_16Dec04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aca61394 cDNA enco	Aad59938 Human kin	Ado40591 Human kin	Aad26454 Human kin	Abz68726 Nucleotid	Abz68725 Nucleotid	Aad38864 Human kin	Ada05643 Human NOV	Abq78871 Human kin	Aal55217 Human CRI	Abg78870 Human kin		Aal55215 Human CRI	Aad39191 Human MDP	Adf60992 Pain asso	Adq89099 Human uro	Adn62808 Human NOV	Adf60993 ORF of pa	Adj96544 Human cit	Aas06701 Polynucle
SUMMARIES	ΙD	ACA61394	AAD59938	ADO40591	AAD26454	ABZ68726	ABZ68725	AAD38864	ADA05643	ABQ78871	AAL55217	ABQ78870	AAL55214	AAL55215	AAD39191	ADF60992	ADQ89099	ADN62808	ADF60993	ADJ96544	AAS06701
	DB	8	10	12	9	10	10	9	8	9	σ	9	σ	σ	9	10	13	12	10	12	4
	Length DB	1515	1515	1515	2066	1765	1485	6298	1870	5877	6156	6165	6165	8603	6574	6574	6574	1870	6162	8656	6129
	& Query Match	100.0	100.0	100.0	99.7	99.4	97.8	92.7	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.1	91.9	91.6	91.2
	Score	1515	1515	1515	1510.2	1505.8	1481.8	1404.2	1398.2	1398.2	1398.2	1398.2	1398.2	1398.2	1397.8	1397.8	1397.8	1395	1391.8	1388	1382
	Result No.	П	7	9	4	S	9	7	8	9	10	11	12	13	14	15	16	17	18	19	20

Abs63436 RHO/RAC-1	Ada05641 Human NOV	Adn62806 Human NOV	Abs63435 Human cDN	Ada05653 Human NOV	Adn62818 Human NOV	Abz68776 Nucleotid	Abx71191 Novel hum	Adn62729 Human cit	Aas79753 DNA encod	Adj79946 Human kin	Abv30132 Human pro	Abv15823 Human pro	Abv45624 Human pro	Abt33346 NOVX DNA	Abt33347 NOVX DNA	Aad38845 Human kin	Adp47966 Human MRC	Adf95101 Human ser	Adf95099 Human ser	Aad30567 Human kin	Adq15093 Human can	Adj96545 Human dys	Juman	Adc99116 Human KPP	
ABS63436	ADA05641	ADN62806	ABS63435	ADA05653	ADN62818	ABZ68776	ABX71191	ADN62729	AAS79753	ADJ79946	ABV30132	ABV15823	ABV45624	ABT33346	ABT33347	AAD38845	ADP47966	ADF95101	ADF95099	AAD30567	ADQ15093	ADJ96545	ADI40903	ADC99116	
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1375.8	1375.8	1375.8	1375.8	1375.8	1375.8	1158	963.2	955.4	940.8	760.8	578.8	441.8	434.4	247.2	247.2	246.8	246.8	246.8	246.8	246.8	246.8	246.8	246.8	246.8	
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ALIGNMENTS

Human; 88; gene; gene therapy; kinase; antisense. 1..6 7..1500 /*tag= b /product= "Kinase" 1501..1515 /*tag= c Location/Qualifiers cDNA encoding novel human kinase. ACA61394 standard; cDNA; 1515 BP. 11-AUG-2003 (first entry) Homo sapiens. ACA61394; Key 5'UTR 3'UTR RESULT 1 ACA61394 SOS

US2003022340-A1.

30-JAN-2003.

11-SEP-2002; 2002US-00238709

13-MAR-2001; 2001US-00804471.

(APPL-) APPLERA CORP.

Webster M, Yan C, Di Francesco V, Beasley EM;

WPI; 2003-438978/41. P-PSDB; ABU10126.

New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.

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The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic proteins, and serve as targets for the development of human therapeutic proteins. The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for monitoring the effectiveness of modulating compounds on the expression or activity of the transporter gene in clinical trials or in treatment regimen, in gene therapy and as antisense constructs to control transporter gene expression in cells, tissue and organisms. The present
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 Score 1515;
Pred. No. 0;
Query Match
Best Local Similarity 100.0%;
Matches 1515; Conservative 0
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RESULT 4

AAD26454;

AAD26454 standard; cDNA; 2066 BP

26-MAR-2002

(first entry) Human kinase PKIN-7 cDNA. Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AlDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; cod pasture's syndrome; Graves' disease; pancreatitis; peoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardiovascular disease; hypertemalon; vasculitis; myocarditis; obesity; congestive heart failure; ischemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy; ss.

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Homo sapiens

/*tag= a /product= "Human PKIN-7 protein" Location/Qualifiers 14. 1507 /*tag= a

WO200196547-A2

20-DEC-2001

14-JUN-2001; 2001WO-US019444.

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The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition associated with decreased expression of treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, anaemia, allergies, adult respiratory distress syndrome, atherosclerosis, ancein, bronchitis, Crohn's disease, disbetes (mellitus, multiple sclerosis, Good pasture's syndrome, graves' disease, osteoarthritis, osteoporosis, pancreatitis, portasis Reiter's syndrome, relativist, using Syndrome, uverits, ulcerative colitis, contentating Sidgen's syndrome, uverits, ulcerative colitis, contentating Sidgen's syndrome, uverity protozoal and helminthic infections) concertis, syndrome, hypothyroidism, cerebral palsy, actarateds; cartariosis, congestive heart failure, angina pectoris, myocarditis, aneurysms, congestive heart failure, angina pectoris, myocarditis, congestive heart failure, angina pectoris, myocarditis, dischaemic heart disease, chronic bronchitis, lumg tumours); lipid disease, chronic bronchitis, lowers, and disease, hypocholesterolaemia, obesity). PRN DNA is useful for assessing toxicity of a test compound and in gene therapy. The present sequence is human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.
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                                                                                                                                                                                                                        Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Rearney L, Burford N, Nguyen DB, Tang YT; Baughn MR, He A, Thornton M, Hafalla A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 180-181; 197pp; English.
15-JUN-2000; 2000US-0213467P.
23-JUN-2000; 2000US-0213467P.
30-JUN-2000; 2000US-02165631P.
07-JUL-2000; 2000US-0218672P.
25-AUG-2000; 2000US-0218972P.
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Best Local Similarity 99.8%;
Matches 1512; Conservative
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P-PSDB; AAE16261.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human citron rho/rac-interacting kinase-short kinase polypeptide and polymuclectide for preventing or treating diseases associated with the polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary disease.
                                                          Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.
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10-DEC-2001; 2001US-0337130P.
25-APR-2002; 2002US-0375015P.
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PR 25-APR-2002; 2002US-0375015P.

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PARE DAYER AG.
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Zhu Z;
Zhu Z;
Zhu Z;
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WPI; 2003-221595/21.

DR P-PSDB; ABP976B1.
XX
New human citron rho/rac-interacting kinase-short kinase polypeptide and polypeptide for preventing or treating diseases associated with the polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary disease.
XX
New human citron rho/rac-interacting kinase-properties of the polypeptide of properties of the present sequence encodes a human citron rho/rac-interacting kinase-short kinase polypeptide. The polynucleotide and polypeptide of the invention are useful in preventing, ameliorating, or treating diseases cased with the polypeptide dysfunction. The expression vector or the reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase-short kinase in a ctivity of a human citron rho/rac-interacting kinase-short kinase in a cc disease, such as obesity or chronic obstructive pulmonary disease. These comorbidities, such as hypertension, diabetes, coronary artery disease. CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep companea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced fertility, and depression
XX
Sequence 1485 BP; 373 A; 353 C; 372 G; 387 T; 0 U; 0 Other;
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Sequence 1485 BP; 373 A; 353 C; 372 G; 387 T; 0 U; 0 Other; Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1483; Conservative 0; Mismatches 2; Indels 0;

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acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertensis; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hIV; neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic; hyperlipidaemia; enzyme; gene; ss.
Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;
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Homo sapiens

/*tag= a /product= "Human kinase (PKIN)-21" Location/Qualifiers 55. .6219 /*tag= a

WO200233099-A2

25-APR-2002

20-OCT-2001; 2001WO-US047728

2000US-0242410P 2000US-0244068P

2000US-0245708P. 2000US-0247672P. 2000US-0249565P. 2000US-0252730P. 20-OCT-2000; 2 27-OCT-2000; 2 03-NOV-2000; 2 09-NOV-2000; 2 22-NOV-2000; 01-DEC-2000;

(INCY-) INCYTE GENOMICS INC.

La] Arvizu C; Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C; Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB; Gandhi AR, Lu Y, Yu Bu.ford, Bandman O, Tribouley CM, Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A; Gandhi AR, Lu Y, Yue H, Burford I Recipon SA, Lu DAM, Borowsky ML, Thangavelu K, Khan FA, Ison CH;

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WPI; 2002-454603/48.

P-PSDB; AAE24150.

New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders.

5; Page 207-209; 210pp; English. claim

The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing, cureating and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma, atherosclerosis, multiple sclerosis, psoriasis), disorders affecting growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis), cardiovascular disorder (e.g., hypertension, myocardial infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver, Goodpasture's disease, Niemann-Pick's disease, hypercholesterolaemia, hyperlipidaemia, obesity), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a diagnostic test for a condition or a disease associated with the expression of PKIN in a composition comprising PKIN or an agonist or antagonist of PKIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN.

The proteome of a tissue or cell type. PKIN DNA is useful for creating the proteome of a tissue or cell type. PKIN DNA is useful for creating checkin humanised animals or transgenic animals to model human diseases.

The proteome of a tissue or cell type. PKIN DNA is useful for creating and in somatic or germline gene therapy. The present sequence is human proteome. PKIN CDNA

Sequence 6298 BP; 1772 A; 1585 C; 1720 G; 1221 T; 0 U; 0 Other;

1080 1020 1068 1008 408 108 120 168 180 228 240 288 300 348 360 420 468 480 528 540 588 900 648 9 708 720 780 828 840 900 948 960 768 888 9 49 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA CCCATTGCCAACCGGGCCTCCAGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 109 CCCATTGCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG Grcadaagrcrrgradgrrgradrcacrrrgcrdaagrgcaggrggradaagagagaaga ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG GGAGGGGACTTGCTGTCTTTTGAATAGATATGAGGACCAGTTAGATGAAACCTGATA GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT CAGCGGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 169 ACTCAACAGCAGATGTCTCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 229 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG AAGTATTCCGACACACATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCA **ACCGGGGACATCTATGCTATGAAGTGAAGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG** GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC CAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT CAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT GGAGGGGACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGGTA CAGTITITACCTAGCTGAGCTGATITITGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 649 CAGTTTTACCTAGCTGAGCTGATTTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGC 829 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGAGTGTGATGAACGGGGATGGAAAAAGGC 841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTAT ACCTACGGCCTGGACTGTGGTGAGTGGCGGGGTTGCCTATGAGATGATTAT GGGAGATCCCCCTTCGCAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 949 GGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTTC cagcegriringaaarinccagargaccccaaagrgagcagcagrgacrircrrgarcrgarr CAAAGCTTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT Gaps ö Indels 3 Mismatches ö Matches 1406; Conservative 121 241 289 301 349 (361 409 529 589 889 961 61 421 469 1021 181 481 541 709 169 901 601 661 721 781 셤 ద ద 쉱 ò 음 g g g 요 g 셤 ઠે ò ò 8 8 ઠે 8 8 ઠ ઠે 유 ઠ 셤 ઠ 셤 8 셤 8 셤 8 셤 8 8

Length 6298; . 9 B Score 1404.2; Pred. No. 0; 92.7%; Query Match Best Local Similarity

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TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACC 1140
              CTCAAGTCTGACGATGACACCTCCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCA 1248
                                                                                                 TCCTCTCCCGGCCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 1260
                                                                                                               ITTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG 1320
                                                                                                                                                                                                   GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGTTCTTCATCAAAAGCAAAGGCTA 1380
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                                                                                                                                                                  TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTTGTGTCGGGTCTG
                                                CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                                                                                     CAAGACTCTCAGGACAAGTGTCACAAGGT 1409
                                                                                                                                                                                                                                                                            1429 CAAGACTCTCAGGACAAGTGTCACAAGAT 1457
                                                                                                                                                                                                                                                                                                                                                                                                                    Human NOV1b encoding cDNA SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "NOV1b"
                                                                                                                                                                                                                                                                                                                                          ADA05643 standard; cDNA; 1870 BP
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2001US-0328056P.
2001US-0328849P.
2001US-0329414P.
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2001US-0327917P.
2001US-0328029P.
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2001US-0330309P.
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09-OCT-2001; 2
12-OCT-2001; 2
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18-0CT-2001;
22-0CT-2001;
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The present into accribed to the properties of the present into present into present into present into present into accribed above and a carrier; (2) a kit composition comprising a polypeptide described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell composition the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above comprising an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or berrant physiological interactions of the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or betraing for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) methods of the activity of the polypeptide; (12) a method for modulating cor preventing a pathology associated with the above polypeptide. Novx sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The copypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic.
                                                                                                                                                                                                                                                                                                                                  Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes NOVX proteins, where X can be 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20, Page 100; 586pp; English.
                                   2002US-0373826P
2002US-037484P
2002US-037497P
2002US-0381037P
2002US-0381038P
2002US-0381042P
2002US-0381642P
2002US-0381642P
2002US-038381E
2002US-0383831P
                                                                                                                                                                                                                                                       2002US-00262511
                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
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                                                                               22-APR-2002;
16-MAY-2002;
16-MAY-2002;
                                                                                                                                                                                                                                                       01-OCT-2002;
                                                                19-APR-2002;
                                                                                                                                             16-MAY-2002;
                                                                                                                                                                   17-MAY-2002;
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                                       19-APR-2002;
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Gaps

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Indels

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DB 8; Length 1870;

Score 1398.2; Pred. No. 0; Pred. No. 0; 0; Mismatches

Query Match Best Local Similarity 99.8%; Matches 1400; Conservative

Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;

the present invention

2001US-0341058P

2001US-0346357P

01-NOV-2001; 17-APR-2002;

disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence encodes a human NOVX protein from

disorders such as Alzheimer's disease or Parkinson'

neurodegenerative

1273

1206 1213 1326 1333 1386

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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine Kinases, particularly Citron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides have a use in gene therapy. The encoded novel polypeptides are useful
                                                                                                                                                                                                                          Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;
Citron rho-interacting kinase; gene therapy; mental disorder; cancer;
                                                                                                             CCGTGCCAGCTCAGCCCCTCAGGCTTCTCGGGGGAAGAACTGCCGTTTGTGGGGGTTTTCG
                                                                                                                                                                   TACAGCAAGGCACTGGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCC
                                                                                                                                                                                          1274 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGGTCTGGACTCC
TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAG
                1094 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCCACCCTCAAG
                                                      TCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT
                                                                        1154 TCTGACGATGACACTCCCAATTTTGATGAACCAGAGAATTCGTGGGGTTTCATCCTCT
                                                                                                                                         1214 ccereccaecreaeccercaecerreresesasasaacreecerrreresestrree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynuclectide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, in therapy of disorders and diseases e.g. cancer and pharmacogenomic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 44-45; 50pp; English.
                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .5877
/*tag= a
/product= "Kinase"
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Anorectic; hypotensive; cardiant, antilipaemic; cerebroprotective; antiquot; osteopathic; antiarthritic; cytostatic; antidepressant; immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic; neuroprotective; antidiabetic; antidiabetic; analgesic; human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating; obesity; comorbidities; cancer; anorexia; cachexia; bulimia; central nervous system disorder; chronic obstructive pulmonary disease; diabetes; pain; ds.
                                                                                                                                                                                                                       CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAAGAACTGCCGTTTGTGGGGTTTTTCG
TTTTTGABAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATCAAAGC
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 generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence encodes a novel·human kinase of the invention
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Pred. No. 0;
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Best Local Similarity 99.8%;
Matches 1400; Conservative (
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547 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT

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The invention relates to an isolated polyphoticolide and numan citron rho/rac-interacting kinase polypeptide. The isolated polymucleotide comprises a 6165 or 8603 base pair sequence, given in the polymucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK)

polypeptide and polymucleotide are useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction such as obesity associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, ostetae and colon cancer).

Cc cancer including endometrial, breast, prostate and colon cancer).

Cc anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease or Alzheimer's clisorders, anxiety disorders, Parkinson's disease or Alzheimer's clisoreders, anxiety disorders, Parkinson's disease or Alzheimer's polypeptide is also useful in diagnostic assays or in genetic testing.

CThe expression vector or the reagent is useful in preparing a medicament of modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polymicleotide and polypeptide and in soreming for agents that modulate the activity of the human CRIK polypeptide. This polymucleotide sequence represents a DNA sequence represents a DNA sequence relating to the human CRIK protein of the invention
New human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or
                                                                                                                                                                                                                               invention relates to an isolated polynucleotide encoding a human
                                                                                                                                                                 Disclosure; Page 217-222; 237pp; English
                                                                                                Alzheimer's disease
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Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;

300 186 246 420 486 480 546 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGG 540 126 120 180 240 306 366 360 426 99 9 GACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCCAGGAGCAGGTTTCA ATGITICAAGTICAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT GCCAACCGGGCCTCCAGGCTGAATCTGTTCCAGGGGAAACCACCCTTTATGACTCAA GCCAGCCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA CAGCAGATGTCTCCTTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAA CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA GAATGCAGTCAGCCTGCTCTGATGAGGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA TCCGACACATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA TITITIGAGGAAGAGGGGAACATATTATCTCGAAGCACAAGGCCCGTGGATCCCCCAATTA CAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGG GACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCCAGGAGCAGGTTTCA TTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA Gaps Length 6156; ö 3; Indels DB 9; Score 1398.2; Pred. No. 0; 0; Mismatches 92.3%; Query Match Best Local Similarity 99.8 Matches 1400; Conservative 247 241 61 121 181 301 361 487 67 127 187 307 367 427 421 181 셤 임 셤 g 셤 유 셤 g à ሯ ઠ 8 ò Š 8 ઠ ⋩

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly Citron tho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polymucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NMP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The
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                                                                                                                                                                                                                                                                                                                                                             /standard_name= "Single nucleotide polymorphism"
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Pred. No. 0;
0; Mismatches
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                                                                                                     Location/Qualifiers
1. .6165
                                                                                                                                                         /*tag= a /product= "Kinase" replace(5218,G) /*tag= /standard_name= "Si replace(6065,G) /*tag= /stag= /stag=
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Best Local Similarity 99.8%;
Matches 1400; Conservative 0
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New human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or
                                                                                                                                                              Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective; antigout; osteopathic; antiarthritic; cytostatic; antidepressant; immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic; neuroprotective; antiinflammatory; antidiabetic; analgesic; human citron rho/rac-interacting kinase; carzyme; CRIK; ameliorating; obesity; comorbidities; cancer; anorexia; cachexia; bulimia; central nervous system disorder; chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .6165
/*tag= a /product= "Human CRIK protein"
                                                                                                                                           Human CRIK encoding DNA sequence, SEQ ID No 1.
                     1403
TCTCAGGACAAGTGTCACAAGGT 1409
            TCTCAGGACAAGTGTCACAAGAT
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11-DEC-2001; 2001US-0338651P.
25-APR-2002; 2002US-0375014P.
                                                                         AAL55214 standard; DNA; 6165
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CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polymucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This polymucleotide sequence represents a DNA sequence encoding a human CRIK protein of the invention
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                                                                                                                                      92.3%; Score 1398.2; DB 9; Length 6165; 99.8%; Pred. No. 0;
                                                                                                      Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;
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The invention relates to an isolated polynuclectide encoding a human citron rho/rac-interacting kinase polypeptide. The isolated polynuclectide comprises a 616 or 8603 base pair sequence, given in the specification. The human citron ho/rac-interacting kinase (CRIK) polypeptide and polynuclectide are useful in preventing, ameliorating, creating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, protester and colon cancer), anorexia, cachexia, bullimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease or Alzheimer's classes), chronic obstructive pullmonary disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in disgnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a

Example 1; Fig 1; 237pp; English

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Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective; antigout; osteopathic; antiarthritic; cytostatic; antidepressant; immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic; neuroprotective; antihnflammatory; antidiabetic; analgesic; human citron rho/rac-interacting kinase; enzyme; CRIK; amellorating; obesity; comorbidities, cancer; anorexia; cachexia; bulimia; central nervous system disorder; chronic obstructive pulmonary disease; Human CRIK related DNA sequence, SEQ ID No 4. BP AAL55215 standard; DNA; 8603 (first entry) 01-MAY-2003 RESULT **AAL5521**

diabetes; pain; ds WO2003004523-A1. sapiens 16-JAN-2003 Ношо

2001US-0338651P. 2001US-0338651P. 2002US-0375014P. 28-JUN-2002; 2002WO-EP007156 02-JUL-2001; 2 11-DEC-2001; 2 25-APR-2002; 2

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BAYER

(FARB) Zhu Z; WPI; 2003-221576/21

citron tho/rac-interacting kinase polypeptide. The isolated polymuclacotide comprises to an isolated polypeptide. The isolated polymuclactide comprises of 165 or 8603 base pair sequence, given in the polymuclactide comprises of 165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK) to polypeptide and polymuclacide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, prostate and colon cancer).

CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, parkinson's disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK colypeptide is also useful in diagnostic assays or in genetic testing.

CT he expression vector or the reagent is useful in preparing a medicament contract nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a cuseful in producing and detecting the polymetering and polypeptide and for use in various assay systems. The methods are contral in producing and detecting the polymetecitie and polypeptide and con agents that modulate the activity of the human CRIK polypeptide. This polymetide sequence represents a DNA sequence correlating to the human CRIK protein of the invention New human citron rho/rac-interacting kinase (CRIK) polypeptide and polymuclectide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or invention relates to an isolated polynucleotide encoding a human Disclosure; Fig 4; 237pp; English Alzheimer's disease.

Gaps DB 9; Length 8603; .; 0 Sequence 8603 BP; 2305 A; 2206 C; 2215 G; 1877 T; 0 U; 0 Other; 3; Indels Query Match 92.3%; Score 1398.2; Best Local Similarity 99.8%; Pred. No. 0; Matches 1400; Conservative 0; Mismatches

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7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT

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/*tag= a
19. .6180
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/product= "Human MDPK protein"
e 19. .6177
/*tag= c
/note= "This region is specifically referred in claim 1
as SEQ ID NO:3"
6181. .6574
/*tag= d
 skeletal muscle disorder; muscular dystrophy; myotonic dystrophy;
immune disorder; neoplastic disorder; gene therapy; gene; ss.
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P-PSDB; AAE24079.
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           GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT
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                                                                                                                                                                                                                The invention relates to human myotonic dystrophy type protein kinase (MDPK) polypeptides designated as 13245 and nucleic acid molecules encoding such polypeptides. 13245 molecules are used to develop diagnostic and therapeutic agents for prognosticating, diagnosing, preventing, inhibiting, alleviating or curing MDPK-related disorders. Polypeptides of the invention are used to develop diagnostic and therapeutic agents for 1345-mediated or related disorders use tumour growth, tumour metastasis, viral infection of a cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies), immune disorders and neoplastic disorders. The invention is also used in
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Human myotonic dystrophy type protein kinase polypeptide and polynucleotide useful for prognosticating, diagnosing, preventing inhibiting tumorigenesis, tumor growth, tumor metastasis and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.3%; Score 1397.8; DB 6; Length 6574; Best Local Similarity 99.5%; Pred. No. 0; Matches 1402; Conservative 0; Mismatches 7; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6574 BP; 1877 A; 1611 C; 1776 G; 1310 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy. The present sequence is human MDPK cDNA
                                                                                                                                                        Claim 1; Fig 1; 148pp; English.
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Human, myotonic dystrophy type protein kinase; MDPK, 13245 protein, tumourigenesis; tumour growth; tumour metastasis; viral infection;

(first entry)

04-OCT-2002

AAD39191;

Human MDPK CDNA

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The present invention relates to a method for identifying a compound capable of modulating pain or painful disorders. The method comprises assaying the ability of the compound to modulate specific nucleic acid expression or polypeptide activity eg. potassium channel, or kinase expression/activity. The method and compounds are useful for treating pain or painful disorders e.g. inflammatory pain, chronic pain, neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache pain and tissue pain. The present sequence encodes a human protein
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                                                                                                                                                                                                                                                                                                                                                                                                Pain modulation; pain disorder; painful disorder; potassium channel; kinase expression; inflammatory pain; chronic pain; neuropathic pain; causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain; analgesic; antlinflammatory; gene; ds.
               GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGCTGAAA
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99.5%; Pred. No. 0;
iive 0; Mismatches
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1 (bases 1 to 1515)
Webster, M., Yan, C., Di Francesco, V. and Beasley, E.M.
Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof Patent: US 6479269-A 112-NOV-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches
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(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Patent: WO 01096547-A 33 20-DEC-2001;
Incyte Genomics, Inc. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RESULT 4
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Homo sapiens (human)

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Regulation of human citron rho/rac-interacting kinase-short
Retent: WO 03004629-A B 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.9%;
Matches 1507; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Regulation of human citron rho/rac-interacting kinase-short Patent: WO 03004629-A 1 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location(Qualifiers
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ROTYGLDCDWWSUGYLAYEMI YGRSPFAEGETSARTFNNI MNFORFLKFPDDFKVSSDF

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AKLEK INBEQULK AKGAFERA VKAGTER TELLON I RQAKERREBELEK LONDREDS

SEGTRKKL VERBELLERKHREAQVSAQHLEVHLKQKEGHYBERKI RVLLDNDGKEDFBEST

TLENMMQRHEDERAHEKGKI LLSEQKAMI NAMDSKI RSLEGRI VELSEANKLAANSSLFT

TLENMMQRHEDERAHEKGKI LLSEQKAMI NAMDSKI RSLEGRI VELSEANKLAANSSLFT
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RLREVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQAKTELEET
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1 (bases 1 to 8576)

Huang, C.Q., Wu, S.L., Shan, Y.X., Liu, S. and Xiao, P.J.

Submitted (18-MAR-2003) Department of Biochemistry and Molecular Biology, Basic Medicine, Suzhou University, Renming Road 48, Suzhou, Jiangsu 215007, China Location/Qualifiers

1. 8576

//crganism="Homo, sapiens"
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54. .6137
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RSPEHQPSAMSLLAPPSSRRKESSTPEEFSRRLKERMHANIPHRFNVGLINMAATKCAV
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Query Match

720

780

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GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT

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Best Local Similarity 99.6%; Pred. No. 0;
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Bukaryoziens

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mac, Y., Xie, Y. and Wu, Q.

Cloning and characterizing a novel human CRIK-SK gene

Unpublished

2 (bases 1 to 1799)

Mac, Y., Xie, Y. and Wu, Q.

Diases 1 to 1799)

Mac, Y., Xie, Y. and Wu, Q.

Direct Submission

Submitted (02-JAN-2003) Institute of Genetics, Fudan University,

20 Handan Road, Shanghai 200433, P.R. China
                                                                                                                                                                   GGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="protein kinase"
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421 421 481 541 541	TACCTAGCTGAGCTGATTTTGGCTGTTCACAGGGTTCATCTGATGGGATACGTGCATCGA GACCTACATCAGGGATACGTGCATTCACGTGCATCGATGGGGATACGTGCATTCATCAGGGATACGTGCATTCAGGTGGATTTT 7	Qy 727 GGATCTGCCGCGAAAATGAATTCAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786	Qy 847 GGCCTGGACTGGTGGTCAGTGGGGGGTGATTGCCTATGACATGATTATGGGAGA 906 bb 841 GGCCTGGACTGGTGGTCAGTGGTGATTGCCTATGAGTTATGGGAGA 900 Qy 907 TCCCCCTTCGCAGAGGAACCTCTGCCAGACCTTCAATAACATTATGAATTTCCAGCGG 966 Db 901 TCCCCCTTCGCAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966 Db 901 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCCAATAACATTATGAATTTCCAGCGG 960	Oy 967 TITITGAAATTICCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026	1021 TTGTTGTGCGGCCAGAAGAGAGCTGAAGTTTGAAGGTCTTTGCTGCATCCTTCTTC 108 1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCTTCTT 108 1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAG 114 1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCCCACCCTCAAG 114	Oy 1147 TCCGACGATGACATTTTGATGAACCAGAGAATTCGTGGGTTTCATCTCT 1206 Db 1141 TCTGACGATGACCCTCCAATTTGATGAACAGAAGAATTCGTGGGTTTCATCTCT 1200 Oy 1207 CCGACGACGACCTCAGGCTCAGGCTTCGGGTGAGAACTTCTGTGGGGTTTTCATCTTT 1200	1201	0y 1327 CCTGCCAAGACTAGGAAAGAAATTCTCATCAAAGGCAAGACTACAAAGC 1380 	RESULT 11 AX671112 LOCUS AX671112 6156 bp DNA linear PAT 27-MAR-2003 DEFINITION Sequence 8 from Patent W003004523.
Qy 1207 CCGTGCCAGCTGAGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1266 Db 1201 CCGTGCCAGCTGAGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTTCG 1260 Qy 1267 TACAGCAAGCCATGGGGATTCTTGGTAGATCTGTGTCGGGTTTGTGCAGCTTTTTCG 1326 Db 1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGTTGTGTCGGGTCTGGACTCC 1320 Qy 1327 CCTGCCAAGACTAGGAAAAGAAACTTCTCAATCAAAGCAAAGAGCTACAAGAC 1386 Db 1321 CCTGCCAAGACTAGCTAGGAAAAGAAACTTCTCATCAAAGCAAAGACTACAAAGC Db 1321 CCTGCCAAGACTAGCAAAAGAAACTTCTCATCAAAAGCAAAGACTACAAAGC 1380	Qy 1387 TCTCAGGACAAGTGTCACAAGGT 1409	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 AUTHORS Yu,X., Miranda,M. and Friddle,C.J. TITLE Human kinases and polymucleotides encoding the same JOURNAL Patent: WO 02059125-A 3 01-AUG-2002; Lexicon Genetics Incorporated (US) FEATURES Location/Qualifiers	<pre>source 15877 /organ="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN</pre>	Query Match 92.3%; Score 1398.2; DB 6; Length 5877; Best Local Similarity 99.8%; Pred. No. 0; Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0; 7 ATGITGAAGITCAAATATGGAGGGGGGAATCCITTGGATGCTGGTGCTGAACCCAIT 66	1 AIGITGAAGITCAAAIAIGGAGCGCGGAAICCITIGGAIGCIGGIGCIGCIGGIGCGCGTTAIGACCCAAIT 67 GCCAACCGGGCCTCCAGGCTGAAICTGITCTTCCAGGGGAAACCACCTTTAIGACTCAA 61 GCCAGCCGGGCCTCCAGGCTGAAICTGITCTTCCAGGGGAACCACCTTTAIGACTCAA	Qy 127 CAGCAGATGTCTCTTTCCCAGAAAGGATATTAGATGCCTTTGTTCTTTGAA 186 Db 121 CAGCAGATGTCTCCTCTTTCCCGAGAAGGATATTAGATGCCTCTTTGTTCTCTTTGAA 180 Qy 187 GAATGCAGTCACCTGCTTAGAAGATTAAGCAGTGAGAACTTTGTCCGGAAGTAT 246 Db 181 [Db 183 GAATGCAGCTCACCTCTCAATGAAGAATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 240		QY 367 GACATCTATGCTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTCA 426

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1 (bases 1 to 6165)
Yu,X.S., Miranda,M. and Friddle,C.J.
Human kinases and polymucleotides encoding
Patent: US 6734009-A 1 11-MAY-2004;
Location/Qualifiers
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                                                    Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Regulation of human citron rho/rac-interacting kinase Patent: WO 03004523-A 8 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Pred. No. 0;
0; Mismatches

    .6156
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

               GI:29329572
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Best Local Similarity 99.8%;
Matches 1400; Conservative
                                         Homo sapiens (human)
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1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGCTGCTGAACCCATT 60 67 GCCAACCGGGCCTCCAGGCTGAATCTTTCCAGGGGAAACCACCTTTATGACTCAA 126 61 GCCAGCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATGACTCAA 120 62 GCCAGACGGGCCTCCAGGCTGAATCTGTTCTTCTTATGACTCAA 120 63 GCCAGATGTCTCCTTTCCCGAGAAGGGATATTAGATGCCCTTTTGTTCTCTTTGAA 180 64 GCCAGATGTCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180 65 GCCAGATGTCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180 66 GCCAGATGTCACCTTTCCCGAGAAGGATATTAGATGCCCTCTTTTGTATCTTTTGAA 180 67 GCCACACCAGTCACCTTTCCCGAGAAGAATTAGATGCCCTTTTTTTT	
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Catarrhini; Hominidae; Homo.
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Zhu,Z.
Regulation of human citron rho/rac-interacting kinase
Patent: WO 03004523-A 1 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Pred. No. 0;
0; Mismatches

    ..6165
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                           AX671105 6165 bp
Sequence 1 from Patent WO03004523
                                                                                          Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                      AX671105
AX671105.1 GI:29329569
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               GACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGCCCCAGGAGCAGGTTTCA
                                                   TTTTTGAGGAAGAGGGAACATATTATCTCGAAGCACAAGCCCGTCGATCCCCCAATTA
                                                                      TTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA
                                                                                                                                                           GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Regulation of human citron rho/rac-interacting kinase Patent: WO 03004523-A 4 16-7AN-2003;
Bayer Aktiengesellschaft (DE)
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                                                                                ATGTTGAAGTTCAAATATGGAGGGGGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT
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                                                              <u> ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT</u>
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Score 1398.2;
Pred. No. 0;
0; Mismatches
92.3%;
                  Best Local Similarity 99.8 Matches 1400; Conservative
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Search completed: March 19, 2005, 11:54:27 Job time : 6461.94 secs